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CERTIFICATE OF MAILING (37 CFR 1.8 (a)).

I hereby certify that the attached papers or fee is being deposited with the United States Postal Service on the date shown below with sufficient postage as first class mail in an envelope addressed to: «INSERT» Assistant Commissioner For Patents, Washington, D.C.

December 6, 1996 Liza D. Hohenschutz
(Date) (Printed Name)

Liza D. Hohenschutz
(Signature)

ZENECA Inc.
Docket No. 70086

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Application of: WOOD ET AL

Serial No.: 08/669,656

Filed: JUNE 24, 1996

For: ION CHANNEL

Box Missing Part
Assistant Commissioner for Patents
Washington, DC 20231

Sir:

**STATEMENT TO SUPPORT FILING AND SUBMISSION
IN ACCORDANCE WITH 37 CFR §§1.821 THROUGH 1.825**

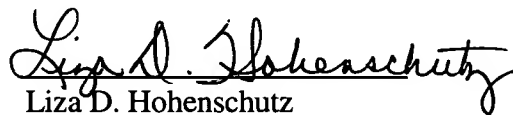
- (X) I hereby state, in accordance with the requirements of **37 C.F.R. §1.821(f)**, that the contents of the paper and computer readable copies of the Sequence Listing, submitted in accordance with the **37 C.F.R. §1.821(c)** and (e), respectively are the same.
- () I hereby state that the submission filed in accordance with **37 C.F.R. 1.821(g)** does not include new matter.
- () I hereby state that the submission filed in accordance with **37 C.F.R. §1.821(h)** does not include new matter or go beyond the disclosure in the international application as filed.
- (X) I hereby state that the amendments, made in accordance with **37 C.F.R. §1.825(a)**, included in the substitute sheet(s) of the Sequence Listing are supported in the

application, as filed, at pages 50-105. I hereby state that the substitute sheet(s) of the Sequence Listing does (do) not include new matter.

- (X) I hereby state that the substitute copy of the computer readable form, submitted in accordance with 37 C.F.R. §1.825(b), is the same as the amended Sequence Listing.
- () I hereby state that the substitute copy of the computer readable form, submitted in accordance with 37 C.F.R. §1.85(d), contains identical data to that originally filed.

Respectfully submitted,

ZENECA INC.



Liza D. Hohenschutz
Attorney for Applicant(s)
Reg. No. 33,712
Telephone: 302/886-7466

Dated: *December 6, 1996*

SEQUENCE LISTING

(1) GENERAL INFORMATION:

5

(i) APPLICANT: Wood, John N.
Akopian, Armen N.

10

(ii) TITLE OF INVENTION: Ion Channel

(iii) NUMBER OF SEQUENCES: 31

15

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: ZENECA Pharmaceuticals
(B) STREET: 1800 Concord Pike, P.O. Box 15437
(C) CITY: Wilmington
(D) STATE: Delaware
(E) COUNTRY: USA
(F) ZIP: 19850

20

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

25

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:
(B) FILING DATE:
(C) CLASSIFICATION:

30

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Hohenschutz, Liza D.
(B) REGISTRATION NUMBER: 33,712
(C) REFERENCE/DOCKET NUMBER: PHM.70086

35

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (302) 886-7466

40

(2) INFORMATION FOR SEQ ID NO:1:

45

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 6524 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

50

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

55

(A) NAME/KEY: CDS
(B) LOCATION: 204..6077

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

60

TAGCTTGCTT CTGCTAATGC TACCCAGGC CTTTAGACAG AGAACAGATG GCAGATGGAG

60

TTTCTTATTG CCATGCGCAA ACGCTGAGCC CACCTCATGA TCCCGGACCC CATGGTTTTC

120

AGTAGACAAC CTGGGCTAAG AAGAGATCTC CGACCTTATA GAGCAGCAA GAGTGTAAT

180

	TCTTCCCCAA	GAAGAATGAG	AAG	ATG	GAG	CTC	CCC	TTT	GCG	TCC	GTG	GGA		230			
				Met	Glu	Leu	Pro	Phe	Ala	Ser	Val	Gly					
				1				5									
5	ACT	ACC	AAT	TTC	AGA	CGG	TTC	ACT	CCA	GAG	TCA	CTG	GCA	GAG	ATC	GAG	278
	Thr	Thr	Asn	Phe	Arg	Arg	Phe	Thr	Pro	Glu	Ser	Leu	Ala	Glu	Ile	Glu	
	10					15					20					25	
10	AAG	CAG	ATT	GCT	GCT	CAC	CGC	GCA	GCC	AAG	AAG	GCC	AGA	ACC	AAG	CAC	326
	Lys	Gln	Ile	Ala	Ala	His	Arg	Ala	Ala	Lys	Lys	Ala	Arg	Thr	Lys	His	
					30					35					40		
15	AGA	GGA	CAG	GAG	GAC	AAG	GGC	GAG	AAG	CCC	AGG	CCT	CAG	CTG	GAC	TTG	374
	Arg	Gly	Gln	Glu	Asp	Lys	Gly	Glu	Lys	Pro	Arg	Pro	Gln	Leu	Asp	Leu	
				45					50					55			
20	AAA	GAC	TGT	AAC	CAG	CTG	CCC	AAG	TTC	TAT	GGT	GAG	CTC	CCA	GCA	GAA	422
	Lys	Asp	Cys	Asn	Gln	Leu	Pro	Lys	Phe	Tyr	Gly	Glu	Leu	Pro	Ala	Glu	
			60					65					70				
25	CTG	GTC	GGG	GAG	CCC	CTG	GAG	GAC	CTA	GAC	CCT	TTC	TAC	AGC	ACA	CAC	470
	Leu	Val	Gly	Glu	Pro	Leu	Glu	Asp	Leu	Asp	Pro	Phe	Tyr	Ser	Thr	His	
		75				80						85					
30	CGG	ACA	TTC	ATG	GTG	TTG	AAT	AAA	AGC	AGG	ACC	ATT	TCC	AGA	TTC	AGT	518
	Arg	Thr	Phe	Met	Val	Leu	Asn	Lys	Ser	Arg	Thr	Ile	Ser	Arg	Phe	Ser	
	90					95					100					105	
35	GCC	ACT	TGG	GCC	CTG	TGG	CTC	TTC	AGT	CCC	TTC	AAC	CTG	ATC	AGA	AGA	566
	Ala	Thr	Trp	Ala	Leu	Trp	Leu	Phe	Ser	Pro	Phe	Asn	Leu	Ile	Arg	Arg	
				110						115					120		
40	ACA	GCC	ATC	AAA	GTG	TCT	GTC	CAT	TCC	TGG	TTC	TCC	ATA	TTC	ATC	ACC	614
	Thr	Ala	Ile	Lys	Val	Ser	Val	His	Ser	Trp	Phe	Ser	Ile	Phe	Ile	Thr	
				125					130					135			
45	ATC	ACT	ATT	TTG	GTC	AAC	TGC	GTG	TGC	ATG	ACC	CGA	ACT	GAT	CTT	CCA	662
	Ile	Thr	Ile	Leu	Val	Asn	Cys	Val	Cys	Met	Thr	Arg	Thr	Asp	Leu	Pro	
		140					145						150				
50	GAG	AAA	GTC	GAG	TAC	GTC	TTC	ACT	GTC	ATT	TAC	ACC	TTC	GAG	GCT	CTG	710
	Glu	Lys	Val	Glu	Tyr	Val	Phe	Thr	Val	Ile	Tyr	Thr	Phe	Glu	Ala	Leu	
		155				160						165					
55	ATT	AAG	ATA	CTG	GCA	AGA	GGG	TTT	TGT	CTA	AAT	GAG	TTC	ACT	TAT	CTT	758
	Ile	Lys	Ile	Leu	Ala	Arg	Gly	Phe	Cys	Leu	Asn	Glu	Phe	Thr	Tyr	Leu	
		170				175				180						185	
60	CGA	GAT	CCG	TGG	AAC	TGG	CTG	GAC	TTC	AGT	GTC	ATT	ACC	TTG	GCG	TAT	806
	Arg	Asp	Pro	Trp	Asn	Trp	Leu	Asp	Phe	Ser	Val	Ile	Thr	Leu	Ala	Tyr	
				190						195				200			
65	GTG	GGT	GCA	GCG	ATA	GAC	CTC	CGA	GGA	ATC	TCA	GCG	CTG	CGG	ACA	TTC	854
	Val	Gly	Ala	Ala	Ile	Asp	Leu	Arg	Gly	Ile	Ser	Gly	Leu	Arg	Thr	Phe	
				205					210				215				
70	CGA	GTT	CTC	AGA	GCC	CTG	AAA	ACT	GTT	TCT	GTG	ATC	CCA	GGA	CTG	AAG	902
	Arg	Val	Leu	Arg	Ala	Leu	Lys	Thr	Val	Ser	Val	Ile	Pro	Gly	Leu	Lys	
			220				225						230				
75	GTC	ATC	GTG	GGA	GCC	CTG	ATC	CAC	TCA	GTG	AGG	AAG	CTG	GCC	GAC	GTG	950
	Val	Ile	Val	Gly	Ala	Leu	Ile	His	Ser	Val	Arg	Lys	Leu	Ala	Asp	Val	
		235				240						245					

	ACT	ATC	CTC	ACA	GTC	TTC	TGC	CTG	AGC	GTC	TTC	GCC	TTG	GTG	GGC	CTG	998
	Thr	Ile	Leu	Thr	Val	Phe	Cys	Leu	Ser	Val	Phe	Ala	Leu	Val	Gly	Leu	
	250					255					260					265	
5	CAG	CTC	TTT	AAG	GGG	AAC	CTT	AAG	AAC	AAA	TGC	ATC	AGG	AAC	GGA	ACA	1046
	Gln	Leu	Phe	Lys	Gly	Asn	Leu	Lys	Asn	Lys	Cys	Ile	Arg	Asn	Gly	Thr	
					270					275					280		
10	GAT	CCC	CAC	AAG	GCT	GAC	AAC	CTC	TCA	TCT	GAA	ATG	GCA	GAA	TAC	GTC	1094
	Asp	Pro	His	Lys	Ala	Asp	Asn	Leu	Ser	Ser	Glu	Met	Ala	Glu	Tyr	Val	
					285				290					295			
15	TCC	ATC	AAG	CCT	GGT	ACT	ACG	GAT	CCC	TTA	CTG	TGC	GGC	AAT	GGG	TCT	1142
	Ser	Ile	Lys	Pro	Gly	Thr	Thr	Asp	Pro	Leu	Leu	Cys	Gly	Asn	Gly	Ser	
			300					305					310				
20	GAT	GCT	GGT	CAC	TGC	CCT	GGA	GGC	TAT	GTC	TGC	CTG	AAA	ACT	CCT	GAC	1190
	Asp	Ala	Gly	His	Cys	Pro	Gly	Gly	Tyr	Val	Cys	Leu	Lys	Thr	Pro	Asp	
		315					320					325					
25	AAC	CCG	GAT	TTT	AAC	TAC	ACC	AGC	TTT	GAT	TCC	TTT	GCG	TGG	GCA	TTC	1238
	Asn	Pro	Asp	Phe	Asn	Tyr	Thr	Ser	Phe	Asp	Ser	Phe	Ala	Trp	Ala	Phe	
		330				335					340					345	
30	CTC	TCA	CTG	TTC	CGC	CTC	ATG	ACG	CAG	GAC	TCC	TGG	GAG	CGC	CTG	TAC	1286
	Leu	Ser	Leu	Phe	Arg	Leu	Met	Thr	Gln	Asp	Ser	Trp	Glu	Arg	Leu	Tyr	
					350					355					360		
35	CAG	CAG	ACA	CTC	CGG	GCT	TCT	GGG	AAA	ATG	TAC	ATG	GTC	TTT	TTC	GTG	1334
	Gln	Gln	Thr	Leu	Arg	Ala	Ser	Gly	Lys	Met	Tyr	Met	Val	Phe	Phe	Val	
				365					370					375			
40	CTG	GTT	ATT	TTC	CTT	GGA	TCG	TTC	TAC	CTG	GTC	AAT	TTG	ATC	TTG	GCC	1382
	Leu	Val	Ile	Phe	Leu	Gly	Ser	Phe	Tyr	Leu	Val	Asn	Leu	Ile	Leu	Ala	
			380					385					390				
45	GTG	GTC	ACC	ATG	GCG	TAT	GAA	GAG	CAG	AGC	CAG	GCA	ACA	ATT	GCA	GAA	1430
	Val	Val	Thr	Met	Ala	Tyr	Glu	Glu	Gln	Ser	Gln	Ala	Thr	Ile	Ala	Glu	
		395					400					405					
50	ATC	GAA	GCC	AAG	GAA	AAA	AAG	TTC	CAG	GAA	GCC	CTT	GAG	GTG	CTG	CAG	1478
	Ile	Glu	Ala	Lys	Glu	Lys	Lys	Phe	Gln	Glu	Ala	Leu	Glu	Val	Leu	Gln	
		410				415					420				425		
55	AAG	GAA	CAG	GAG	GTG	CTG	GCA	GCC	CTG	GGG	ATT	GAC	ACG	ACC	TCG	CTC	1526
	Lys	Glu	Gln	Glu	Val	Leu	Ala	Ala	Leu	Gly	Ile	Asp	Thr	Thr	Ser	Leu	
					430					435					440		
60	CAG	TCC	CAC	AGT	GGA	TCA	CCC	TTA	GCC	TCC	AAA	AAC	GCC	AAT	GAG	AGA	1574
	Gln	Ser	His	Ser	Gly	Ser	Pro	Leu	Ala	Ser	Lys	Asn	Ala	Asn	Glu	Arg	
				445				450						455			
65	AGA	CCC	AGG	GTG	AAA	TCA	AGG	GTG	TCA	GAG	GGC	TCC	ACG	GAT	GAC	AAC	1622
	Arg	Pro	Arg	Val	Lys	Ser	Arg	Val	Ser	Glu	Gly	Ser	Thr	Asp	Asp	Asn	
			460					465						470			
70	AGG	TCA	CCC	CAA	TCT	GAC	CCT	TAC	AAC	CAG	CGC	AGG	ATG	TCT	TTC	CTA	1670
	Arg	Ser	Pro	Gln	Ser	Asp	Pro	Tyr	Asn	Gln	Arg	Arg	Met	Ser	Phe	Leu	
		475					480					485					
75	GGC	CTG	TCT	TCA	GGA	AGA	CGC	AGG	GCT	AGC	CAC	GGC	AGT	GTG	TTC	CAC	1718
	Gly	Leu	Ser	Ser	Gly	Arg	Arg	Arg	Ala	Ser	His	Gly	Ser	Val	Phe	His	
		490				495					500					505	

	TTC	CGA	GCG	CCC	AGC	CAA	GAC	ATC	TCA	TTT	CCT	GAC	GGG	ATC	ACC	CCT	1766
	Phe	Arg	Ala	Pro	Ser	Gln	Asp	Ile	Ser	Phe	Pro	Asp	Gly	Ile	Thr	Pro	
5					510					515					520		
	GAT	GAT	GGG	GTC	TTT	CAC	GGA	GAC	CAG	GAA	AGC	CGT	CGA	GGT	TCC	ATA	1814
	Asp	Asp	Gly	Val	Phe	His	Gly	Asp	Gln	Glu	Ser	Arg	Arg	Gly	Ser	Ile	
				525					530					535			
10	TTG	CTG	GGC	AGG	GGT	GCT	GGG	CAG	ACA	GGT	CCA	CTC	CCC	AGG	AGC	CCA	1862
	Leu	Leu	Gly	Arg	Gly	Ala	Gly	Gln	Thr	Gly	Pro	Leu	Pro	Arg	Ser	Pro	
			540					545					550				
15	CTG	CCT	CAG	TCC	CCC	AAC	CCT	GGC	CGT	AGA	CAT	GGA	GAA	GAG	GGA	CAG	1910
	Leu	Pro	Gln	Ser	Pro	Asn	Pro	Gly	Arg	Arg	His	Gly	Glu	Glu	Gly	Gln	
		555					560					565					
20	CTC	GGA	GTG	CCC	ACT	GGT	GAG	CTT	ACC	GCT	GGA	GCG	CCT	GAA	GGC	CCG	1958
	Leu	Gly	Val	Pro	Thr	Gly	Glu	Leu	Thr	Ala	Gly	Ala	Pro	Glu	Gly	Pro	
	570					575					580					585	
25	GCA	CTG	CAC	ACT	ACA	GGG	CAG	AAG	AGC	TTC	CTG	TCT	GCG	GGC	TAC	TTG	2006
	Ala	Leu	His	Thr	Thr	Gly	Gln	Lys	Ser	Phe	Leu	Ser	Ala	Gly	Tyr	Leu	
					590					595					600		
	AAC	GAA	CCT	TTC	CGA	GCA	CAG	AGG	GCC	ATG	AGC	GTT	GTC	AGT	ATC	ATG	2054
	Asn	Glu	Pro	Phe	Arg	Ala	Gln	Arg	Ala	Met	Ser	Val	Val	Ser	Ile	Met	
				605					610					615			
30	ACT	TCT	GTC	ATT	GAG	GAG	CTT	GAA	GAG	TCT	AAG	CTG	AAG	TGC	CCA	CCC	2102
	Thr	Ser	Val	Ile	Glu	Glu	Leu	Glu	Glu	Ser	Lys	Leu	Lys	Cys	Pro	Pro	
			620					625					630				
35	TGC	TTG	ATC	AGC	TTC	GCT	CAG	AAG	TAT	CTG	ATC	TGG	GAG	TGC	TGC	CCC	2150
	Cys	Leu	Ile	Ser	Phe	Ala	Gln	Lys	Tyr	Leu	Ile	Trp	Glu	Cys	Cys	Pro	
		635					640					645					
40	AAG	TGG	AGG	AAG	TTC	AAG	ATG	GCG	CTG	TTC	GAG	CTG	GTG	ACT	GAC	CCC	2198
	Lys	Trp	Arg	Lys	Phe	Lys	Met	Ala	Leu	Phe	Glu	Leu	Val	Thr	Asp	Pro	
	650					655					660					665	
45	TTC	GCA	GAG	CTT	ACC	ATC	ACC	CTC	TGC	ATC	GTG	GTG	AAC	ACC	GTC	TTC	2246
	Phe	Ala	Glu	Leu	Thr	Ile	Thr	Leu	Cys	Ile	Val	Val	Asn	Thr	Val	Phe	
					670					675					680		
	ATG	GCC	ATG	GAG	CAC	TAC	CCC	ATG	ACC	GAT	GCC	TTC	GAT	GCC	ATG	CTT	2294
	Met	Ala	Met	Glu	His	Tyr	Pro	Met	Thr	Asp	Ala	Phe	Asp	Ala	Met	Leu	
				685					690				695				
50	CAA	GCC	GGC	AAC	ATT	GTC	TTC	ACC	GTG	TTT	TTC	ACA	ATG	GAG	ATG	GCC	2342
	Gln	Ala	Gly	Asn	Ile	Val	Phe	Thr	Val	Phe	Phe	Thr	Met	Glu	Met	Ala	
			700					705					710				
55	TTC	AAG	ATC	ATT	GCC	TTC	GAC	CCC	TAC	TAT	TAC	TTC	CAG	AAG	AAG	TGG	2390
	Phe	Lys	Ile	Ile	Ala	Phe	Asp	Pro	Tyr	Tyr	Tyr	Phe	Gln	Lys	Lys	Trp	
		715					720					725					
60	AAT	ATC	TTC	GAC	TGT	GTC	ATC	GTC	ACC	GTG	AGC	CTT	CTG	GAG	CTG	AGT	2438
	Asn	Ile	Phe	Asp	Cys	Val	Ile	Val	Thr	Val	Ser	Leu	Leu	Glu	Leu	Ser	
	730					735					740					745	
	GCA	TCC	AAG	AAG	GGC	AGC	CTG	TCT	GTG	CTC	CGT	ACC	TTA	CGC	TTG	CTG	2486
	Ala	Ser	Lys	Lys	Gly	Ser	Leu	Ser	Val	Leu	Arg	Thr	Leu	Arg	Leu	Leu	
					750					755					760		

	CGG	GTC	TTC	AAG	CTG	GCC	AAG	TCC	TGG	CCC	ACC	CTG	AAC	ACC	CTC	ATC	2534
	Arg	Val	Phe	Lys	Leu	Ala	Lys	Ser	Trp	Pro	Thr	Leu	Asn	Thr	Leu	Ile	
				765					770					775			
5	AAG	ATC	ATC	GGG	AAC	TCA	GTG	GGG	GCC	CTG	GGC	AAC	CTG	ACC	TTT	ATC	2582
	Lys	Ile	Ile	Gly	Asn	Ser	Val	Gly	Ala	Leu	Gly	Asn	Leu	Thr	Phe	Ile	
				780				785					790				
10	CTG	GCC	ATC	ATC	GTC	TTC	ATC	TTC	GCC	CTG	GTC	GGA	AAG	CAG	CTT	CTC	2630
	Leu	Ala	Ile	Ile	Val	Phe	Ile	Phe	Ala	Leu	Val	Gly	Lys	Gln	Leu	Leu	
		795					800					805					
15	TCA	GAG	GAC	TAC	GGG	TGC	CGC	AAG	GAC	GGC	GTC	TCC	GTG	TGG	AAC	GGC	2678
	Ser	Glu	Asp	Tyr	Gly	Cys	Arg	Lys	Asp	Gly	Val	Ser	Val	Trp	Asn	Gly	
	810					815					820					825	
20	GAG	AAG	CTC	CGC	TGG	CAC	ATG	TGT	GAC	TTC	TTC	CAT	TCC	TTC	CTG	GTC	2726
	Glu	Lys	Leu	Arg	Trp	His	Met	Cys	Asp	Phe	Phe	His	Ser	Phe	Leu	Val	
					830					835					840		
25	GTC	TTC	CGA	ATC	CTC	TGC	GGG	GAG	TGG	ATC	GAG	AAC	ATG	TGG	GTC	TGC	2774
	Val	Phe	Arg	Ile	Leu	Cys	Gly	Glu	Trp	Ile	Glu	Asn	Met	Trp	Val	Cys	
				845					850					855			
30	ATG	GAG	GTC	AGC	CAG	AAA	TCC	ATC	TCC	CTC	ATC	CTC	TTC	TTG	ACT	GTG	2822
	Met	Glu	Val	Ser	Gln	Lys	Ser	Ile	Cys	Leu	Ile	Leu	Phe	Leu	Thr	Val	
			860					865					870				
35	ATG	GTG	CTG	GGC	AAC	CTA	GTG	GTG	CTC	AAC	CTT	TTC	ATC	GCT	TTA	CTG	2870
	Met	Val	Leu	Gly	Asn	Leu	Val	Val	Leu	Asn	Leu	Phe	Ile	Ala	Leu	Leu	
		875					880					885					
40	CTG	AAC	TCC	TTC	AGC	GCG	GAC	AAC	CTC	ACG	GCT	CCA	GAG	GAT	GAC	GGG	2918
	Leu	Asn	Ser	Phe	Ser	Ala	Asp	Asn	Leu	Thr	Ala	Pro	Glu	Asp	Asp	Gly	
	890					895					900					905	
45	GAG	GTG	AAC	AAC	TTG	CAG	TTA	GCA	CTG	GCC	AGG	ATC	CAG	GTA	CTT	GGC	2966
	Glu	Val	Asn	Asn	Leu	Gln	Leu	Ala	Leu	Ala	Arg	Ile	Gln	Val	Leu	Gly	
					910					915				920			
50	CAT	CGG	GCC	AGC	AGG	GCC	AGC	GCC	AGT	TAC	ATC	AGC	AGC	CAC	TGC	CGA	3014
	His	Arg	Ala	Ser	Arg	Ala	Ser	Ala	Ser	Tyr	Ile	Ser	Ser	His	Cys	Arg	
				925					930					935			
55	TTC	CAC	TGG	CCC	AAG	GTG	GAG	ACC	CAG	CTG	GGC	ATG	AAG	CCC	CCA	CTC	3062
	Phe	His	Trp	Pro	Lys	Val	Glu	Thr	Gln	Leu	Gly	Met	Lys	Pro	Pro	Leu	
			940					945					950				
60	ACC	AGC	TCA	GAG	GCC	AAG	AAC	CAC	ATT	GCC	ACT	GAT	GCT	GTC	AGT	GCT	3110
	Thr	Ser	Ser	Glu	Ala	Lys	Asn	His	Ile	Ala	Thr	Asp	Ala	Val	Ser	Ala	
		955					960					965					
65	GCA	GTG	GGG	AAC	CTG	ACA	AAG	CCA	GCT	CTC	AGT	AGC	CCC	AAG	GAG	AAC	3158
	Ala	Val	Gly	Asn	Leu	Thr	Lys	Pro	Ala	Leu	Ser	Ser	Pro	Lys	Glu	Asn	
	970					975					980					985	
70	CAC	GGG	GAC	TTC	ATC	ACT	GAT	CCC	AAC	GTG	TGG	GTC	TCT	GTG	CCC	ATT	3206
	His	Gly	Asp	Phe	Ile	Thr	Asp	Pro	Asn	Val	Trp	Val	Ser	Val	Pro	Ile	
					990					995					1000		
75	GCT	GAG	GGG	GAA	TCT	GAC	CTC	GAC	GAG	CTC	GAG	GAA	GAT	ATG	GAG	CAG	3254
	Ala	Glu	Gly	Glu	Ser	Asp	Leu	Asp	Glu	Leu	Glu	Glu	Asp	Met	Glu	Gln	
				1005					1010					1015			

	GCT	TCG	CAG	AGC	TCC	TGG	CAG	GAA	GAG	GAC	CCC	AAG	GGA	CAG	CAG	GAG	3302
	Ala	Ser	Gln	Ser	Ser	Trp	Gln	Glu	Glu	Asp	Pro	Lys	Gly	Gln	Gln	Glu	
			1020					1025					1030				
5	CAG	TTG	CCA	CAA	GTC	CAA	AAG	TGT	GAA	AAC	CAC	CAG	GCA	GCC	AGA	AGC	3350
	Gln	Leu	Pro	Gln	Val	Gln	Lys	Cys	Glu	Asn	His	Gln	Ala	Ala	Arg	Ser	
			1035				1040					1045					
10	CCA	GCC	TCC	ATG	ATG	TCC	TCT	GAG	GAC	CTG	GCT	CCA	TAC	CTG	GGT	GAG	3398
	Pro	Ala	Ser	Met	Met	Ser	Ser	Glu	Asp	Leu	Ala	Pro	Tyr	Leu	Gly	Glu	
						1055					1060					1065	
15	AGC	TGG	AAG	AGG	AAG	GAT	AGC	CCT	CAG	GTC	CCT	GCC	GAG	GGA	GTG	GAT	3446
	Ser	Trp	Lys	Arg	Lys	Asp	Ser	Pro	Gln	Val	Pro	Ala	Glu	Gly	Val	Asp	
					1070					1075					1080		
20	GAC	ACG	AGC	TCC	TCT	GAG	GGC	AGC	ACG	GTG	GAC	TGC	CCG	GAC	CCA	GAG	3494
	Asp	Thr	Ser	Ser	Ser	Glu	Gly	Ser	Thr	Val	Asp	Cys	Pro	Asp	Pro	Glu	
				1085				1090						1095			
25	GAA	ATC	CTG	AGG	AAG	ATC	CCC	GAG	CTG	GCA	CAT	GAC	CTG	GAC	GAG	CCC	3542
	Glu	Ile	Leu	Arg	Lys	Ile	Pro	Glu	Leu	Ala	His	Asp	Leu	Asp	Glu	Pro	
			1100				1105						1110				
30	GAT	GAC	TGT	TTC	AGA	GAA	GGC	TGC	ACT	CGC	CGC	TGT	CCC	TGC	TGC	AAC	3590
	Asp	Asp	Cys	Phe	Arg	Glu	Gly	Cys	Thr	Arg	Arg	Cys	Pro	Cys	Cys	Asn	
			1115				1120					1125					
35	GTG	AAT	ACT	AGC	AAG	TCT	CCT	TGG	GCC	ACA	GGC	TGG	CAG	GTG	CGC	AAG	3638
	Val	Asn	Thr	Ser	Lys	Ser	Pro	Trp	Ala	Thr	Gly	Trp	Gln	Val	Arg	Lys	
						1135				1140						1145	
40	ACC	TGC	TAC	CGC	ATC	GTG	GAG	CAC	AGC	TGG	TTT	GAG	AGT	TTC	ATC	ATC	3686
	Thr	Cys	Tyr	Arg	Ile	Val	Glu	His	Ser	Trp	Phe	Glu	Ser	Phe	Ile	Ile	
					1150					1155					1160		
45	TTC	ATG	ATC	CTG	CTC	AGC	AGT	GGA	GCG	CTG	GCC	TTT	GAG	GAT	AAC	TAC	3734
	Phe	Met	Ile	Leu	Leu	Ser	Ser	Gly	Ala	Leu	Ala	Phe	Glu	Asp	Asn	Tyr	
				1165				1170					1175				
50	CTG	GAA	GAG	AAA	CCC	CGA	GTG	AAG	TCC	GTG	CTG	GAG	TAC	ACT	GAC	CGA	3782
	Leu	Glu	Glu	Lys	Pro	Arg	Val	Lys	Ser	Val	Leu	Glu	Tyr	Thr	Asp	Arg	
			1180					1185					1190				
55	GTG	TTC	ACC	TTC	ATC	TTC	GTC	TTT	GAG	ATG	CTG	CTC	AAG	TGG	GTA	GCC	3830
	Val	Phe	Thr	Phe	Ile	Phe	Val	Phe	Glu	Met	Leu	Leu	Lys	Trp	Val	Ala	
			1195				1200					1205					
60	TAT	GGC	TTC	AAA	AAG	TAT	TTC	ACC	AAT	GCC	TGG	TGC	TGG	CTG	GAC	TTC	3878
	Tyr	Gly	Phe	Lys	Lys	Tyr	Phe	Thr	Asn	Ala	Trp	Cys	Trp	Leu	Asp	Phe	
						1215					1220					1225	
65	CTC	ATT	GTG	AAC	ATC	TCC	CTG	ACA	AGC	CTC	ATA	GCG	AAG	ATC	CTT	GAG	3926
	Leu	Ile	Val	Asn	Ile	Ser	Leu	Thr	Ser	Leu	Ile	Ala	Lys	Ile	Leu	Glu	
				1230						1235					1240		
70	TAT	TCC	GAC	GTG	GCG	TCC	ATC	AAA	GCC	CTT	CGG	ACT	CTC	CGT	GCC	CTC	3974
	Tyr	Ser	Asp	Val	Ala	Ser	Ile	Lys	Ala	Leu	Arg	Thr	Leu	Arg	Ala	Leu	
				1245				1250					1255				
75	CGA	CCG	CTG	CGG	GCT	CTG	TCT	CGA	TTC	GAA	GGC	ATG	AGG	GTA	GTG	GTG	4022
	Arg	Pro	Leu	Arg	Ala	Leu	Ser	Arg	Phe	Glu	Gly	Met	Arg	Val	Val	Val	
			1260					1265					1270				

	GAT	GCC	CTC	GTG	GGC	GCC	ATC	CCC	TCC	ATC	ATG	AAC	GTC	CTC	CTC	GTC	4070
	Asp	Ala	Leu	Val	Gly	Ala	Ile	Pro	Ser	Ile	Met	Asn	Val	Leu	Leu	Val	
		1275					1280					1285					
5	TGC	CTC	ATC	TTC	TGG	CTC	ATC	TTC	AGC	ATC	ATG	GGC	GTG	AAC	CTC	TTC	4118
	Cys	Leu	Ile	Phe	Trp	Leu	Ile	Phe	Ser	Ile	Met	Gly	Val	Asn	Leu	Phe	
		1290				1295					1300					1305	
10	GCC	GGG	AAA	TTT	TCG	AAG	TGC	GTC	GAC	ACC	AGA	AAT	AAC	CCA	TTT	TCC	4166
	Ala	Gly	Lys	Phe	Ser	Lys	Cys	Val	Asp	Thr	Arg	Asn	Asn	Pro	Phe	Ser	
					1310					1315					1320		
15	AAC	GTG	AAT	TCG	ACG	ATG	GTG	AAT	AAC	AAG	TCC	GAG	TGT	CAC	AAT	CAA	4214
	Asn	Val	Asn	Ser	Thr	Met	Val	Asn	Asn	Lys	Ser	Glu	Cys	His	Asn	Gln	
				1325					1330					1335			
20	AAC	AGC	ACC	GGC	CAC	TTC	TTC	TGG	GTC	AAC	GTC	AAA	GTC	AAC	TTC	GAC	4262
	Asn	Ser	Thr	Gly	His	Phe	Phe	Trp	Val	Asn	Val	Lys	Val	Asn	Phe	Asp	
			1340					1345					1350				
25	AAC	GTC	GCT	ATG	GGC	TAC	CTC	GCA	CTT	CTT	CAG	GTG	GCA	ACC	TTC	AAA	4310
	Asn	Val	Ala	Met	Gly	Tyr	Leu	Ala	Leu	Leu	Gln	Val	Ala	Thr	Phe	Lys	
			1355				1360					1365					
30	GGC	TGG	ATG	GAC	ATA	ATG	TAT	GCA	GCT	GTT	GAT	TCC	GGA	GAG	ATC	AAC	4358
	Gly	Trp	Met	Asp	Ile	Met	Tyr	Ala	Ala	Val	Asp	Ser	Gly	Glu	Ile	Asn	
		1370				1375					1380					1385	
35	AGT	CAG	CCT	AAC	TGG	GAG	AAC	AAC	TTG	TAC	ATG	TAC	CTG	TAC	TTC	GTC	4406
	Ser	Gln	Pro	Asn	Trp	Glu	Asn	Asn	Leu	Tyr	Met	Tyr	Leu	Tyr	Phe	Val	
					1390					1395					1400		
40	GTT	TTC	ATC	ATT	TTC	GGT	GGC	TTC	TTC	ACG	CTG	AAT	CTC	TTT	GTT	GGG	4454
	Val	Phe	Ile	Ile	Phe	Gly	Gly	Phe	Phe	Thr	Leu	Asn	Leu	Phe	Val	Gly	
				1405					1410					1415			
45	GTC	ATA	ATC	GAC	AAC	TTC	AAC	CAA	CAG	AAA	AAA	AAG	CTA	GGA	GGC	CAG	4502
	Val	Ile	Ile	Asp	Asn	Phe	Asn	Gln	Gln	Lys	Lys	Lys	Leu	Gly	Gly	Gln	
			1420					1425					1430				
50	GAC	ATC	TTC	ATG	ACA	GAA	GAG	CAG	AAG	AAG	TAC	TAC	AAT	GCC	ATG	AAG	4550
	Asp	Ile	Phe	Met	Thr	Glu	Glu	Gln	Lys	Lys	Tyr	Tyr	Asn	Ala	Met	Lys	
		1435					1440				1445						
55	AAG	CTG	GGC	TCC	AAG	AAA	CCC	CAG	AAG	CCC	ATC	CGA	CGG	CCC	CTG	AAT	4598
	Lys	Leu	Gly	Ser	Lys	Lys	Pro	Gln	Lys	Pro	Ile	Pro	Arg	Pro	Leu	Asn	
		1450				1455					1460					1465	
60	AAG	TAC	CAA	GGC	TTC	GTG	TTT	GAC	ATC	GTG	ACC	AGG	CAA	GCC	TTT	GAC	4646
	Lys	Tyr	Gln	Gly	Phe	Val	Phe	Asp	Ile	Val	Thr	Arg	Gln	Ala	Phe	Asp	
				1470						1475					1480		
65	ATC	ATC	ATC	ATG	GTT	CTC	ATC	TGC	CTC	AAC	ATG	ATC	ACC	ATG	ATG	GTG	4694
	Ile	Ile	Ile	Met	Val	Leu	Ile	Cys	Leu	Asn	Met	Ile	Thr	Met	Met	Val	
				1485					1490					1495			
70	GAG	ACC	GAC	GAG	CAG	GGC	GAG	GAG	AAG	ACG	AAG	GTT	CTG	GCC	AGA	ATC	4742
	Glu	Thr	Asp	Glu	Gln	Gly	Glu	Glu	Lys	Thr	Lys	Val	Leu	Gly	Arg	Ile	
			1500				1505						1510				
75	AAC	CAG	TTC	TTT	GTG	GCC	GTC	TTC	ACG	GGC	GAG	TGT	GTG	ATG	AAG	ATG	4790
	Asn	Gln	Phe	Phe	Val	Ala	Val	Phe	Thr	Gly	Glu	Cys	Val	Met	Lys	Met	
		1515					1520					1525					

5 TTC GCC CTG CGA CAG TAC TAC TTC ACC AAC GGC TGG AAC GTG TTC GAC 4838
 Phe Ala Leu Arg Gln Tyr Tyr Phe Thr Asn Gly Trp Asn Val Phe Asp
 1530 1535 1540 1545
 10 TTC ATA GTG GTG ATC CTG TCC ATT GGG AGT CTG CTG TTT TCT GCA ATC 4886
 Phe Ile Val Val Ile Leu Ser Ile Gly Ser Leu Leu Phe Ser Ala Ile
 1550 1555 1560
 15 CTT AAG TCA CTG GAA AAC TAC TTC TCC CCG ACG CTC TTC CGG GTC ATC 4934
 Leu Lys Ser Leu Glu Asn Tyr Phe Ser Pro Thr Leu Phe Arg Val Ile
 1565 1570 1575
 20 CGT CTG GCC AGG ATC GGC CGC ATC CTC AGG CTG ATC CGA GCA GCC AAG 4982
 Arg Leu Ala Arg Ile Gly Arg Ile Leu Arg Leu Ile Arg Ala Ala Lys
 1580 1585 1590
 25 GGG ATT CGC ACG CTG CTC TTC GCC CTC ATG ATG TCC CTG CCC GCC CTC 5030
 Gly Ile Arg Thr Leu Leu Phe Ala Leu Met Met Ser Leu Pro Ala Leu
 1595 1600 1605
 30 TTC AAC ATC GGC CTC CTC CTC TTC CTC GTC ATG TTC ATC TAC TCC ATC 5078
 Phe Asn Ile Gly Leu Leu Leu Phe Leu Val Met Phe Ile Tyr Ser Ile
 1610 1615 1620 1625
 35 TTC GGC ATG GCC AGC TTC GCT AAC GTC GTG GAC GAG GCC GGC ATC GAC 5126
 Phe Gly Met Ala Ser Phe Ala Asn Val Val Asp Glu Ala Gly Ile Asp
 1630 1635 1640
 40 GAC ATG TTC AAC TTC AAG ACC TTT GGC AAC AGC ATG CTG TGC CTG TTC 5174
 Asp Met Phe Asn Phe Lys Thr Phe Gly Asn Ser Met Leu Cys Leu Phe
 1645 1650 1655
 45 CAG ATC ACC ACC TCG GCC GGC TGG GAC GGC CTC CTC AGC CCC ATC CTC 5222
 Gln Ile Thr Thr Ser Ala Gly Trp Asp Gly Leu Leu Ser Pro Ile Leu
 1660 1665 1670
 50 AAC ACG GGG CCT CCC TAC TGC GAC CCC AAC CTG CCC AAC AGC AAC GGC 5270
 Asn Thr Gly Pro Pro Tyr Cys Asp Pro Asn Leu Pro Asn Ser Asn Gly
 1675 1680 1685
 55 TCC CGG GGG AAC TGC GGG AGC CCG GCG GTG GGC ATC ATC TTC TTC ACC 5318
 Ser Arg Gly Asn Cys Gly Ser Pro Ala Val Gly Ile Ile Phe Phe Thr
 1690 1695 1700 1705
 60 ACC TAC ATC ATC ATC TCC TTC CTC ATC GTG GTC AAC ATG TAC ATC GCA 5366
 Thr Tyr Ile Ile Ile Ser Phe Leu Ile Val Val Asn Met Tyr Ile Ala
 1710 1715 1720
 65 GTG ATT CTG GAG AAC TTC AAC GTA GCC ACC GAG GAG AGC ACC GAG CCC 5414
 Val Ile Leu Glu Asn Phe Asn Val Ala Thr Glu Glu Ser Thr Glu Pro
 1725 1730 1735
 70 CTG AGC GAG GAC GAC TTC GAC ATG TTC TAT GAG ACC TGG GAG AAG TTC 5462
 Leu Ser Glu Asp Asp Phe Asp Met Phe Tyr Glu Thr Trp Glu Lys Phe
 1740 1745 1750
 75 GAC CCG GAG GCC ACC CAG TTC ATT GCC TTT TCT GCC CTC TCA GAC TTC 5510
 Asp Pro Glu Ala Thr Gln Phe Ile Ala Phe Ser Ala Leu Ser Asp Phe
 1755 1760 1765
 80 GCG GAC ACG CTC TCC GGC CCT CTT AGA ATC CCC AAA CCC AAC CAG AAT 5558
 Ala Asp Thr Leu Ser Gly Pro Leu Arg Ile Pro Lys Pro Asn Gln Asn
 1770 1775 1780 1785

	ATA	TTA	ATC	CAG	ATG	GAC	CTG	CCG	TTG	GTC	CCC	GGG	GAT	AAG	ATC	CAC	5606
	Ile	Leu	Ile	Gln	Met	Asp	Leu	Pro	Leu	Val	Pro	Gly	Asp	Lys	Ile	His	
5					1790					1795					1800		
	TGT	CTG	GAC	ATC	CTT	TTT	GCC	TTC	ACA	AAG	AAC	GTC	TTG	GGA	GAA	TCC	5654
	Cys	Leu	Asp	Ile	Leu	Phe	Ala	Phe	Thr	Lys	Asn	Val	Leu	Gly	Glu	Ser	
					1805				1810					1815			
10	GGG	GAG	TTG	GAC	TCC	CTG	AAG	ACC	AAT	ATG	GAA	GAG	AAG	TTT	ATG	GCG	5702
	Gly	Glu	Leu	Asp	Ser	Leu	Lys	Thr	Asn	Met	Glu	Glu	Lys	Phe	Met	Ala	
					1820			1825						1830			
15	ACC	AAT	CTC	TCC	AAA	GCA	TCC	TAT	GAA	CCA	ATA	GCC	ACC	ACC	CTC	CGG	5750
	Thr	Asn	Leu	Ser	Lys	Ala	Ser	Tyr	Glu	Pro	Ile	Ala	Thr	Thr	Leu	Arg	
					1835			1840					1845				
	TGG	AAG	CAG	GAA	GAC	CTC	TCA	GCC	ACA	GTC	ATT	CAA	AAG	GCC	TAC	CGG	5798
20	Trp	Lys	Gln	Glu	Asp	Leu	Ser	Ala	Thr	Val	Ile	Gln	Lys	Ala	Tyr	Arg	
		1850				1855					1860					1865	
	AGC	TAC	ATG	CTG	CAC	CGC	TCC	TTG	ACA	CTC	TCC	AAC	ACC	CTG	CAT	GTG	5846
	Ser	Tyr	Met	Leu	His	Arg	Ser	Leu	Thr	Leu	Ser	Asn	Thr	Leu	His	Val	
					1870				1875						1880		
25	CCC	AGG	GCT	GAG	GAG	GAT	GGC	GTG	TCA	CTT	CCC	GGG	GAA	GGC	TAC	ATT	5894
	Pro	Arg	Ala	Glu	Glu	Asp	Gly	Val	Ser	Leu	Pro	Gly	Glu	Gly	Tyr	Ile	
					1885			1890						1895			
30	ACA	TTC	ATG	GCA	AAC	AGT	GGA	CTC	CCG	GAC	AAA	TCA	GAA	ACT	GCC	TCT	5942
	Thr	Phe	Met	Ala	Asn	Ser	Gly	Leu	Pro	Asp	Lys	Ser	Glu	Thr	Ala	Ser	
					1900			1905						1910			
	GCT	ACG	TCT	TTC	CCG	CCA	TCC	TAT	GAC	AGT	GTC	ACC	AGG	GGC	CTG	AGT	5990
35	Ala	Thr	Ser	Phe	Pro	Pro	Ser	Tyr	Asp	Ser	Val	Thr	Arg	Gly	Leu	Ser	
			1915				1920					1925					
	GAC	CGG	GCC	AAC	ATT	AAC	CCA	TCT	AGC	TCA	ATG	CAA	AAT	GAA	GAT	GAG	6038
40	Asp	Arg	Ala	Asn	Ile	Asn	Pro	Ser	Ser	Ser	Met	Gln	Asn	Glu	Asp	Glu	
			1930			1935					1940					1945	
	GTC	GCT	GCT	AAG	GAA	GGA	AAC	AGC	CCT	GGA	CCT	CAG	TGAAGGCACT				6084
	Val	Ala	Ala	Lys	Glu	Gly	Asn	Ser	Pro	Gly	Pro	Gln					
					1950					1955							
45	CAGGCATGCA	CAGGGCAGGT	TCCAATGTCT	TTCTCTGCTG	TACTA	ACTCC	TTCCCTCTGG										6144
	AGGTGGCACC	AACCTCCAGC	CTCCACCAAT	GCATGTCACT	GGTCATGGTG	TCAGAACTGA											6204
50	ATGGGGACAT	CCTTGAGAAA	GCCCCACCC	CAATAGGAAT	CAAAAGCCAA	GGATACTCCT											6264
	CCATTCTGAC	GTCCCTTCCG	AGTTCCCGA	AGATGTCATT	GCTCCCTTCT	GTTTGTGACC											6324
	AGAGACGTGA	TTCACCAACT	TCTCGGAGCC	AGAGACACAT	AGCAAAGACT	TTTCTGCTGG											

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1957 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

5 Met Glu Leu Pro Phe Ala Ser Val Gly Thr Thr Asn Phe Arg Arg Phe
 1 5 10 15
 15 Thr Pro Glu Ser Leu Ala Glu Ile Glu Lys Gln Ile Ala Ala His Arg
 20 25 30
 20 Ala Ala Lys Lys Ala Arg Thr Lys His Arg Gly Gln Glu Asp Lys Gly
 35 40 45
 25 Glu Lys Pro Arg Pro Gln Leu Asp Leu Lys Asp Cys Asn Gln Leu Pro
 50 55 60
 30 Lys Phe Tyr Gly Glu Leu Pro Ala Glu Leu Val Gly Glu Pro Leu Glu
 65 70 75 80
 35 Asp Leu Asp Pro Phe Tyr Ser Thr His Arg Thr Phe Met Val Leu Asn
 85 90 95
 40 Lys Ser Arg Thr Ile Ser Arg Phe Ser Ala Thr Trp Ala Leu Trp Leu
 100 105 110
 45 Phe Ser Pro Phe Asn Leu Ile Arg Arg Thr Ala Ile Lys Val Ser Val
 115 120 125
 50 His Ser Trp Phe Ser Ile Phe Ile Thr Ile Thr Ile Leu Val Asn Cys
 130 135 140
 55 Val Cys Met Thr Arg Thr Asp Leu Pro Glu Lys Val Glu Tyr Val Phe
 145 150 155 160
 60 Thr Val Ile Tyr Thr Phe Glu Ala Leu Ile Lys Ile Leu Ala Arg Gly
 165 170 175
 65 Phe Cys Leu Asn Glu Phe Thr Tyr Leu Arg Asp Pro Trp Asn Trp Leu
 180 185 190
 70 Asp Phe Ser Val Ile Thr Leu Ala Tyr Val Gly Ala Ala Ile Asp Leu
 195 200 205
 75 Arg Gly Ile Ser Gly Leu Arg Thr Phe Arg Val Leu Arg Ala Leu Lys
 210 215 220
 80 Thr Val Ser Val Ile Pro Gly Leu Lys Val Ile Val Gly Ala Leu Ile
 225 230 235 240
 85 His Ser Val Arg Lys Leu Ala Asp Val Thr Ile Leu Thr Val Phe Cys
 245 250 255
 90 Leu Ser Val Phe Ala Leu Val Gly Leu Gln Leu Phe Lys Gly Asn Leu
 260 265 270
 95 Lys Asn Lys Cys Ile Arg Asn Gly Thr Asp Pro His Lys Ala Asp Asn
 275 280 285

Leu Ser Ser Glu Met Ala Glu Tyr Val Ser Ile Lys Pro Gly Thr Thr
 290 295 300
 5 Asp Pro Leu Leu Cys Gly Asn Gly Ser Asp Ala Gly His Cys Pro Gly
 305 310 315 320
 Gly Tyr Val Cys Leu Lys Thr Pro Asp Asn Pro Asp Phe Asn Tyr Thr
 325 330 335
 10 Ser Phe Asp Ser Phe Ala Trp Ala Phe Leu Ser Leu Phe Arg Leu Met
 340 345 350
 Thr Gln Asp Ser Trp Glu Arg Leu Tyr Gln Gln Thr Leu Arg Ala Ser
 355 360 365
 15 Gly Lys Met Tyr Met Val Phe Phe Val Leu Val Ile Phe Leu Gly Ser
 370 375 380
 20 Phe Tyr Leu Val Asn Leu Ile Leu Ala Val Val Thr Met Ala Tyr Glu
 385 390 395 400
 Glu Gln Ser Gln Ala Thr Ile Ala Glu Ile Glu Ala Lys Glu Lys Lys
 405 410 415
 25 Phe Gln Glu Ala Leu Glu Val Leu Gln Lys Glu Gln Glu Val Leu Ala
 420 425 430
 Ala Leu Gly Ile Asp Thr Thr Ser Leu Gln Ser His Ser Gly Ser Pro
 435 440 445
 30 Leu Ala Ser Lys Asn Ala Asn Glu Arg Arg Pro Arg Val Lys Ser Arg
 450 455 460
 35 Val Ser Glu Gly Ser Thr Asp Asp Asn Arg Ser Pro Gln Ser Asp Pro
 465 470 475 480
 Tyr Asn Gln Arg Arg Met Ser Phe Leu Gly Leu Ser Ser Gly Arg Arg
 485 490 495
 40 Arg Ala Ser His Gly Ser Val Phe His Phe Arg Ala Pro Ser Gln Asp
 500 505 510
 Ile Ser Phe Pro Asp Gly Ile Thr Pro Asp Asp Gly Val Phe His Gly
 515 520 525
 45 Asp Gln Glu Ser Arg Arg Gly Ser Ile Leu Leu Gly Arg Gly Ala Gly
 530 535 540
 50 Gln Thr Gly Pro Leu Pro Arg Ser Pro Leu Pro Gln Ser Pro Asn Pro
 545 550 555 560
 Gly Arg Arg His Gly Glu Glu Gly Gln Leu Gly Val Pro Thr Gly Glu
 565 570 575
 55 Leu Thr Ala Gly Ala Pro Glu Gly Pro Ala Leu His Thr Thr Gly Gln
 580 585 590
 60 Lys Ser Phe Leu Ser Ala Gly Tyr Leu Asn Glu Pro Phe Arg Ala Gln
 595 600 605
 Arg Ala Met Ser Val Val Ser Ile Met Thr Ser Val Ile Glu Glu Leu
 610 615 620

Glu Glu Ser Lys Leu Lys Cys Pro Pro Cys Leu Ile Ser Phe Ala Gln
 625 630 635 640
 5 Lys Tyr Leu Ile Trp Glu Cys Cys Pro Lys Trp Arg Lys Phe Lys Met
 645 650 655
 Ala Leu Phe Glu Leu Val Thr Asp Pro Phe Ala Glu Leu Thr Ile Thr
 660 665 670
 10 Leu Cys Ile Val Val Asn Thr Val Phe Met Ala Met Glu His Tyr Pro
 675 680 685
 Met Thr Asp Ala Phe Asp Ala Met Leu Gln Ala Gly Asn Ile Val Phe
 690 695 700
 15 Thr Val Phe Phe Thr Met Glu Met Ala Phe Lys Ile Ile Ala Phe Asp
 705 710 715 720
 Pro Tyr Tyr Tyr Phe Gln Lys Lys Trp Asn Ile Phe Asp Cys Val Ile
 725 730 735
 20 Val Thr Val Ser Leu Leu Glu Leu Ser Ala Ser Lys Lys Gly Ser Leu
 740 745 750
 25 Ser Val Leu Arg Thr Leu Arg Leu Leu Arg Val Phe Lys Leu Ala Lys
 755 760 765
 Ser Trp Pro Thr Leu Asn Thr Leu Ile Lys Ile Ile Gly Asn Ser Val
 770 775 780
 30 Gly Ala Leu Gly Asn Leu Thr Phe Ile Leu Ala Ile Ile Val Phe Ile
 785 790 795 800
 Phe Ala Leu Val Gly Lys Gln Leu Leu Ser Glu Asp Tyr Gly Cys Arg
 805 810 815
 35 Lys Asp Gly Val Ser Val Trp Asn Gly Glu Lys Leu Arg Trp His Met
 820 825 830
 40 Cys Asp Phe Phe His Ser Phe Leu Val Val Phe Arg Ile Leu Cys Gly
 835 840 845
 Glu Trp Ile Glu Asn Met Trp Val Cys Met Glu Val Ser Gln Lys Ser
 850 855 860
 45 Ile Cys Leu Ile Leu Phe Leu Thr Val Met Val Leu Gly Asn Leu Val
 865 870 875 880
 50 Val Leu Asn Leu Phe Ile Ala Leu Leu Leu Asn Ser Phe Ser Ala Asp
 885 890 895
 Asn Leu Thr Ala Pro Glu Asp Asp Gly Glu Val Asn Asn Leu Gln Leu
 900 905 910
 55 Ala Leu Ala Arg Ile Gln Val Leu Gly His Arg Ala Ser Arg Ala Ser
 915 920 925
 60 Ala Ser Tyr Ile Ser Ser His Cys Arg Phe His Trp Pro Lys Val Glu
 930 935 940
 Thr Gln Leu Gly Met Lys Pro Pro Leu Thr Ser Ser Glu Ala Lys Asn
 945 950 955 960

His Ile Ala Thr Asp Ala Val Ser Ala Ala Val Gly Asn Leu Thr Lys
 965 970 975
 5 Pro Ala Leu Ser Ser Pro Lys Glu Asn His Gly Asp Phe Ile Thr Asp
 980 985 990
 Pro Asn Val Trp Val Ser Val Pro Ile Ala Glu Gly Glu Ser Asp Leu
 995 1000 1005
 10 Asp Glu Leu Glu Glu Asp Met Glu Gln Ala Ser Gln Ser Ser Trp Gln
 1010 1015 1020
 Glu Glu Asp Pro Lys Gly Gln Gln Glu Gln Leu Pro Gln Val Gln Lys
 1025 1030 1035 1040
 15 Cys Glu Asn His Gln Ala Ala Arg Ser Pro Ala Ser Met Met Ser Ser
 1045 1050 1055
 Glu Asp Leu Ala Pro Tyr Leu Gly Glu Ser Trp Lys Arg Lys Asp Ser
 1060 1065 1070
 Pro Gln Val Pro Ala Glu Gly Val Asp Asp Thr Ser Ser Ser Glu Gly
 1075 1080 1085
 25 Ser Thr Val Asp Cys Pro Asp Pro Glu Glu Ile Leu Arg Lys Ile Pro
 1090 1095 1100
 Glu Leu Ala His Asp Leu Asp Glu Pro Asp Asp Cys Phe Arg Glu Gly
 1105 1110 1115 1120
 30 Cys Thr Arg Arg Cys Pro Cys Cys Asn Val Asn Thr Ser Lys Ser Pro
 1125 1130 1135
 Trp Ala Thr Gly Trp Gln Val Arg Lys Thr Cys Tyr Arg Ile Val Glu
 1140 1145 1150
 35 His Ser Trp Phe Glu Ser Phe Ile Ile Phe Met Ile Leu Leu Ser Ser
 1155 1160 1165
 Gly Ala Leu Ala Phe Glu Asp Asn Tyr Leu Glu Glu Lys Pro Arg Val
 1170 1175 1180
 40 Lys Ser Val Leu Glu Tyr Thr Asp Arg Val Phe Thr Phe Ile Phe Val
 1185 1190 1195 1200
 45 Phe Glu Met Leu Leu Lys Trp Val Ala Tyr Gly Phe Lys Lys Tyr Phe
 1205 1210 1215
 Thr Asn Ala Trp Cys Trp Leu Asp Phe Leu Ile Val Asn Ile Ser Leu
 1220 1225 1230
 50 Thr Ser Leu Ile Ala Lys Ile Leu Glu Tyr Ser Asp Val Ala Ser Ile
 1235 1240 1245
 55 Lys Ala Leu Arg Thr Leu Arg Ala Leu Arg Pro Leu Arg Ala Leu Ser
 1250 1255 1260
 Arg Phe Glu Gly Met Arg Val Val Val Asp Ala Leu Val Gly Ala Ile
 1265 1270 1275 1280
 60 Pro Ser Ile Met Asn Val Leu Leu Val Cys Leu Ile Phe Trp Leu Ile
 1285 1290 1295
 Phe Ser Ile Met Gly Val Asn Leu Phe Ala Gly Lys Phe Ser Lys Cys
 1300 1305 1310

Val Asp Thr Arg Asn Asn Pro Phe Ser Asn Val Asn Ser Thr Met Val
 1315 1320 1325
 5 Asn Asn Lys Ser Glu Cys His Asn Gln Asn Ser Thr Gly His Phe Phe
 1330 1335 1340
 Trp Val Asn Val Lys Val Asn Phe Asp Asn Val Ala Met Gly Tyr Leu
 1345 1350 1355 1360
 10 Ala Leu Leu Gln Val Ala Thr Phe Lys Gly Trp Met Asp Ile Met Tyr
 1365 1370 1375
 Ala Ala Val Asp Ser Gly Glu Ile Asn Ser Gln Pro Asn Trp Glu Asn
 1380 1385 1390
 15 Asn Leu Tyr Met Tyr Leu Tyr Phe Val Val Phe Ile Ile Phe Gly Gly
 1395 1400 1405
 20 Phe Phe Thr Leu Asn Leu Phe Val Gly Val Ile Ile Asp Asn Phe Asn
 1410 1415 1420
 Gln Gln Lys Lys Lys Leu Gly Gly Gln Asp Ile Phe Met Thr Glu Glu
 1425 1430 1435 1440
 25 Gln Lys Lys Tyr Tyr Asn Ala Met Lys Lys Leu Gly Ser Lys Lys Pro
 1445 1450 1455
 Gln Lys Pro Ile Pro Arg Pro Leu Asn Lys Tyr Gln Gly Phe Val Phe
 1460 1465 1470
 30 Asp Ile Val Thr Arg Gln Ala Phe Asp Ile Ile Ile Met Val Leu Ile
 1475 1480 1485
 35 Cys Leu Asn Met Ile Thr Met Met Val Glu Thr Asp Glu Gln Gly Glu
 1490 1495 1500
 Glu Lys Thr Lys Val Leu Gly Arg Ile Asn Gln Phe Phe Val Ala Val
 1505 1510 1515 1520
 40 Phe Thr Gly Glu Cys Val Met Lys Met Phe Ala Leu Arg Gln Tyr Tyr
 1525 1530 1535
 Phe Thr Asn Gly Trp Asn Val Phe Asp Phe Ile Val Val Ile Leu Ser
 1540 1545 1550
 45 Ile Gly Ser Leu Leu Phe Ser Ala Ile Leu Lys Ser Leu Glu Asn Tyr
 1555 1560 1565
 50 Phe Ser Pro Thr Leu Phe Arg Val Ile Arg Leu Ala Arg Ile Gly Arg
 1570 1575 1580
 Ile Leu Arg Leu Ile Arg Ala Ala Lys Gly Ile Arg Thr Leu Leu Phe
 1585 1590 1595 1600
 55 Ala Leu Met Met Ser Leu Pro Ala Leu Phe Asn Ile Gly Leu Leu Leu
 1605 1610 1615
 Phe Leu Val Met Phe Ile Tyr Ser Ile Phe Gly Met Ala Ser Phe Ala
 1620 1625 1630
 60 Asn Val Val Asp Glu Ala Gly Ile Asp Asp Met Phe Asn Phe Lys Thr
 1635 1640 1645

Phe Gly Asn Ser Met Leu Cys Leu Phe Gln Ile Thr Thr Ser Ala Gly
1650 1655 1660

5 Trp Asp Gly Leu Leu Ser Pro Ile Leu Asn Thr Gly Pro Pro Tyr Cys
1665 1670 1675 1680

Asp Pro Asn Leu Pro Asn Ser Asn Gly Ser Arg Gly Asn Cys Gly Ser
1685 1690 1695

10 Pro Ala Val Gly Ile Ile Phe Phe Thr Thr Tyr Ile Ile Ile Ser Phe
1700 1705 1710

Leu Ile Val Val Asn Met Tyr Ile Ala Val Ile Leu Glu Asn Phe Asn
1715 1720 1725

15 Val Ala Thr Glu Glu Ser Thr Glu Pro Leu Ser Glu Asp Asp Phe Asp
1730 1735 1740

20 Met Phe Tyr Glu Thr Trp Glu Lys Phe Asp Pro Glu Ala Thr Gln Phe
1745 1750 1755 1760

Ile Ala Phe Ser Ala Leu Ser Asp Phe Ala Asp Thr Leu Ser Gly Pro
1765 1770 1775

25 Leu Arg Ile Pro Lys Pro Asn Gln Asn Ile Leu Ile Gln Met Asp Leu
1780 1785 1790

30 Pro Leu Val Pro Gly Asp Lys Ile His Cys Leu Asp Ile Leu Phe Ala
1795 1800 1805

Phe Thr Lys Asn Val Leu Gly Glu Ser Gly Glu Leu Asp Ser Leu Lys
1810 1815 1820

35 Thr Asn Met Glu Glu Lys Phe Met Ala Thr Asn Leu Ser Lys Ala Ser
1825 1830 1835 1840

Tyr Glu Pro Ile Ala Thr Thr Leu Arg Trp Lys Gln Glu Asp Leu Ser
1845 1850 1855

40 Ala Thr Val Ile Gln Lys Ala Tyr Arg Ser Tyr Met Leu His Arg Ser
1860 1865 1870

45 Leu Thr Leu Ser Asn Thr Leu His Val Pro Arg Ala Glu Glu Asp Gly
1875 1880 1885

Val Ser Leu Pro Gly Glu Gly Tyr Ile Thr Phe Met Ala Asn Ser Gly
1890 1895 1900

50 Leu Pro Asp Lys Ser Glu Thr Ala Ser Ala Thr Ser Phe Pro Pro Ser
1905 1910 1915 1920

Tyr Asp Ser Val Thr Arg Gly Leu Ser Asp Arg Ala Asn Ile Asn Pro
1925 1930 1935

55 Ser Ser Ser Met Gln Asn Glu Asp Glu Val Ala Ala Lys Glu Gly Asn
1940 1945 1950

60 Ser Pro Gly Pro Gln
1955

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2573 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
(B) LOCATION: 561..2126

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CTGGGAGAGA AAGCGTCTCG CCTAGCGACT CCCAGAGCTT TAAGCCGGGA AGGGACAAGC 60
GTCAGGACAT CTCAGAAATCC CGAACCTTCT AGGGAGGGAG GTTCTTACCT CCATGCTTCC 120
CGTAGGAACC TAATCCCAAT TATTTAGCTG TATTTATAAT ACAAATATG AATGTTAAAT 180
GTACAAATG CTTTCCAGC ATGCCTGCAT CTCCTCCTAG AGTCCTGTTC CCAAGCCCTC 240
TCTACTCTCA GTACTGTAGA AAAGAAATAA GCTTTACGTG AGAAACCCAG GCACTGGATC 300
TTATCCAGGT GCTCACCTCA GAGTCTTTAG TGGGTGTAGC GCTGTGGTAG AGCATTGTGT 360
TATAGATACA AACCAGGGC AGGGAGACTG CAGTGGCCAT TCTCTCCAG GCCAGACGTG 420
CCCTGATCCT TCCCACAGAG ATGAGAAGGC TGGAAACCAGA AACTCAGGT TTTGGCTTCT 480
CTTGGGGGAG GAGAGGTAAT CTTGTTACTT TAATAACATC AGTGTGTCCC TCTCCTCTAC 540
TAGGAGGCCA GGACATCTTC ATG ACA GAA GAG CAG AAG AAG TAC TAC AAT 590
Met Thr Glu Glu Gln Lys Lys Tyr Tyr Asn
1 5 10
GCC ATG AAG AAG CTG GGC TCC AAG AAA CCC CAG AAG CCC ATC CCA CGG 638
Ala Met Lys Lys Leu Gly Ser Lys Lys Pro Gln Lys Pro Ile Pro Arg
15 20 25
CCC CTG AAT AAG TAC CAA GGC TTC GTG TTT GAC ATC GTG ACC AGG CAA 686
Pro Leu Asn Lys Tyr Gln Gly Phe Val Phe Asp Ile Val Thr Arg Gln
30 35 40
GCC TTT GAC ATC ATC ATC ATG GTT CTC ATC TGC CTC AAC ATG ATC ACC 734
Ala Phe Asp Ile Ile Ile Met Val Leu Ile Cys Leu Asn Met Ile Thr
45 50 55
ATG ATG GTG GAG ACC GAC GAG CAG GGC GAG GAG AAG ACG AAG GTT CTG 782
Met Met Val Glu Thr Asp Glu Gln Gly Glu Glu Lys Thr Lys Val Leu
60 65 70
GGC AGA ATC AAC CAG TTC TTT GTG GCC GTC TTC ACG GGC GAG TGT GTG 830
Gly Arg Ile Asn Gln Phe Phe Val Ala Val Phe Thr Gly Glu Cys Val
75 80 85 90
ATG AAG ATG TTC GCC CTG CGA CAG TAC TAC TTC ACC AAC GGC TGG AAC 878
Met Lys Met Phe Ala Leu Arg Gln Tyr Tyr Phe Thr Asn Gly Trp Asn
95 100 105

	GTG	TTC	GAC	TTC	ATA	GTG	GTG	ATC	CTG	TCC	ATT	GGG	AGT	CTG	CTG	TTT	926
	Val	Phe	Asp	Phe	Ile	Val	Val	Ile	Leu	Ser	Ile	Gly	Ser	Leu	Leu	Phe	
				110					115					120			
5	TCT	GCA	ATC	CTT	AAG	TCA	CTG	GAA	AAC	TAC	TTC	TCC	CCG	ACG	CTC	TTC	974
	Ser	Ala	Ile	Leu	Lys	Ser	Leu	Glu	Asn	Tyr	Phe	Ser	Pro	Thr	Leu	Phe	
			125					130					135				
10	CGG	GTC	ATC	CGT	CTG	GCC	AGG	ATC	GGC	CGC	ATC	CTC	AGG	CTG	ATC	CGA	1022
	Arg	Val	Ile	Arg	Leu	Ala	Arg	Ile	Gly	Arg	Ile	Leu	Arg	Leu	Ile	Arg	
		140					145					150					
15	GCA	GCC	AAG	GGG	ATT	CGC	ACG	CTG	CTC	TTC	GCC	CTC	ATG	ATG	TCC	CTG	1070
	Ala	Ala	Lys	Gly	Ile	Arg	Thr	Leu	Leu	Phe	Ala	Leu	Met	Met	Ser	Leu	
	155					160					165					170	
20	CCC	GCC	CTC	TTC	AAC	ATC	GGC	CTC	CTC	CTC	TTC	CTC	GTC	ATG	TTC	ATC	1118
	Pro	Ala	Leu	Phe	Asn	Ile	Gly	Leu	Leu	Leu	Phe	Leu	Val	Met	Phe	Ile	
					175					180					185		
25	TAC	TCC	ATC	TTC	GGC	ATG	GCC	AGC	TTC	GCT	AAC	GTC	GTG	GAC	GAG	GCC	1166
	Tyr	Ser	Ile	Phe	Gly	Met	Ala	Ser	Phe	Ala	Asn	Val	Val	Asp	Glu	Ala	
				190				195						200			
30	GGC	ATC	GAC	GAC	ATG	TTC	AAC	TTC	AAG	ACC	TTT	GGC	AAC	AGC	ATG	CTG	1214
	Gly	Ile	Asp	Asp	Met	Phe	Asn	Phe	Lys	Thr	Phe	Gly	Asn	Ser	Met	Leu	
			205					210					215				
35	TGC	CTG	TTC	CAG	ATC	ACC	ACC	TCG	GCC	GGC	TGG	GAC	GGC	CTC	CTC	AGC	1262
	Cys	Leu	Phe	Gln	Ile	Thr	Thr	Ser	Ala	Gly	Trp	Asp	Gly	Leu	Leu	Ser	
		220					225					230					
40	CCC	ATC	CTC	AAC	ACG	GGG	CCT	CCC	TAC	TGC	GAC	CCC	AAC	CTG	CCC	AAC	1310
	Pro	Ile	Leu	Asn	Thr	Gly	Pro	Pro	Tyr	Cys	Asp	Pro	Asn	Leu	Pro	Asn	
	235					240					245					250	
45	AGC	AAC	GGC	TCC	CGG	GGG	AAC	TGC	GGG	AGC	CCG	GCG	GTG	GGC	ATC	ATC	1358
	Ser	Asn	Gly	Ser	Arg	Gly	Asn	Cys	Gly	Ser	Pro	Ala	Val	Gly	Ile	Ile	
					255					260					265		
50	TTC	TTC	ACC	ACC	TAC	ATC	ATC	ATC	TCC	TTC	CTC	ATC	GTG	GTC	AAC	ATG	1406
	Phe	Phe	Thr	Thr	Tyr	Ile	Ile	Ile	Ser	Phe	Leu	Ile	Val	Val	Asn	Met	
				270					275					280			
55	TAC	ATC	GCA	GTG	ATT	CTG	GAG	AAC	TTC	AAC	GTA	GCC	ACC	GAG	GAG	AGC	1454
	Tyr	Ile	Ala	Val	Ile	Leu	Glu	Asn	Phe	Asn	Val	Ala	Thr	Glu	Glu	Ser	
			285					290				295					
60	ACG	GAG	CCC	CTG	AGC	GAG	GAC	GAC	TTC	GAC	ATG	TTC	TAT	GAG	ACC	TGG	1502
	Thr	Glu	Pro	Leu	Ser	Glu	Asp	Asp	Phe	Asp	Met	Phe	Tyr	Glu	Thr	Trp	
		300					305				310						
65	GAG	AAG	TTC	GAC	CCG	GAG	GCC	ACC	CAG	TTC	ATT	GCC	TTT	TCT	GCC	CTC	1550
	Glu	Lys	Phe	Asp	Pro	Glu	Ala	Thr	Gln	Phe	Ile	Ala	Phe	Ser	Ala	Leu	
	315					320					325					330	
70	TCA	GAC	TTC	GCG	GAC	ACG	CTC	TCC	GGC	CCT	CTT	AGA	ATC	CCC	AAA	CCC	1598
	Ser	Asp	Phe	Ala	Asp	Thr	Leu	Ser	Gly	Pro	Leu	Arg	Ile	Pro	Lys	Pro	
					335					340					345		
75	AAC	CAG	AAT	ATA	TTA	ATC	CAG	ATG	GAC	CTG	CCG	TTG	GTC	CCC	GGG	GAT	1646
	Asn	Gln	Asn	Ile	Leu	Ile	Gln	Met	Asp	Leu	Pro	Leu	Val	Pro	Gly	Asp	
				350					355					360			

AAG ATC CAC TGT CTG GAC ATC CTT TTT GCC TTC ACA AAG AAC GTC TTG 1694
 Lys Ile His Cys Leu Asp Ile Leu Phe Ala Phe Thr Lys Asn Val Leu
 365 370 375
 5 GGA GAA TCC GGG GAG TTG GAC TCC CTG AAG ACC AAT ATG GAA GAG AAG 1742
 Gly Glu Ser Gly Glu Leu Asp Ser Leu Lys Thr Asn Met Glu Glu Lys
 380 385 390
 10 TTT ATG GCG ACC AAT CTC TCC AAA GCA TCC TAT GAA CCA ATA GCC ACC 1790
 Phe Met Ala Thr Asn Leu Ser Lys Ala Ser Tyr Glu Pro Ile Ala Thr
 395 400 405 410
 15 ACC CTC CGG TGG AAG CAG GAA GAC CTC TCA GCC ACA GTC ATT CAA AAG 1838
 Thr Leu Arg Trp Lys Gln Glu Asp Leu Ser Ala Thr Val Ile Gln Lys
 415 420 425
 20 GCC TAC CGG AGC TAC ATG CTG CAC CGC TCC TTG ACA CTC TCC AAC ACC 1886
 Ala Tyr Arg Ser Tyr Met Leu His Arg Ser Leu Thr Leu Ser Asn Thr
 430 435 440
 25 CTG CAT GTG CCC AGG GCT GAG GAG GAT GGC GTG TCA CTT CCC GGG GAA 1934
 Leu His Val Pro Arg Ala Glu Glu Asp Gly Val Ser Leu Pro Gly Glu
 445 450 455
 30 GGC TAC ATT ACA TTC ATG GCA AAC AGT GGA CTC CCG GAC AAA TCA GAA 1982
 Gly Tyr Ile Thr Phe Met Ala Asn Ser Gly Leu Pro Asp Lys Ser Glu
 460 465 470
 35 ACT GCC TCT GCT ACG TCT TTC CCG CCA TCC TAT GAC AGT GTC ACC AGG 2030
 Thr Ala Ser Ala Thr Ser Phe Pro Pro Ser Tyr Asp Ser Val Thr Arg
 475 480 485 490
 40 GGC CTG AGT GAC CGG GCC AAC ATT AAC CCA TCT AGC TCA ATG CAA AAT 2078
 Gly Leu Ser Asp Arg Ala Asn Ile Asn Pro Ser Ser Ser Met Gln Asn
 495 500 505
 GAA GAT GAG GTC GCT GCT AAG GAA GGA AAC AAC CCT GGA CCT CAG TGAAGGCACT 2133
 Glu Asp Glu Val Ala Ala Lys Glu Gly Asn Ser Pro Gly Pro Gln
 510 515 520
 CAGGCATGCA CAGGGCAGGT TCCAATGTCT TTCTCTGCTG TACTAACTCC TTCCCTCTGG 2193
 AGGTGGCACC AACCTCCAGC CTCCACCAAT GCATGTCACCT GGTTCATGGTG TCAGAACTGA 2253
 45 ATGGGGACAT CCTTGAGAAA GCCCCACCC CAATAGGAAT CAAAAGCCAA GGATACTCCT 2313
 CCATTCTGAC GTCCCTTCCG AGTTCCCAGA AGATGTCATT GCTCCCTTCT GTTTGTGACC 2373
 50 AGAGACGTGA TTCACCAACT TCTCGGAGCC AGAGACACAT AGCAAAGACT TTTCTGCTGG 2433
 TGTCGGGCAG TCTTAGAGAA GTCACGTAGG GGTGTTGACT GAGAATTAGG GTTTGCATGA 2493
 CTGCATGCTC ACAGCTGCCG GACAATACCT GTGAGTCGGC CATTAATAATT AATATTTTAA 2553
 55 AAGTTAAAAA AAAAAAAAAA 2573

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 521 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Thr Glu Glu Gln Lys Lys Tyr Tyr Asn Ala Met Lys Lys Leu Gly
1 5 10 15
Ser Lys Lys Pro Gln Lys Pro Ile Pro Arg Pro Leu Asn Lys Tyr Gln
20 25 30
Gly Phe Val Phe Asp Ile Val Thr Arg Gln Ala Phe Asp Ile Ile Ile
35 40 45
Met Val Leu Ile Cys Leu Asn Met Ile Thr Met Met Val Glu Thr Asp
50 55 60
Glu Gln Gly Glu Glu Lys Thr Lys Val Leu Gly Arg Ile Asn Gln Phe
65 70 75 80
Phe Val Ala Val Phe Thr Gly Glu Cys Val Met Lys Met Phe Ala Leu
85 90 95
Arg Gln Tyr Tyr Phe Thr Asn Gly Trp Asn Val Phe Asp Phe Ile Val
100 105 110
Val Ile Leu Ser Ile Gly Ser Leu Leu Phe Ser Ala Ile Leu Lys Ser
115 120 125
Leu Glu Asn Tyr Phe Ser Pro Thr Leu Phe Arg Val Ile Arg Leu Ala
130 135 140
Arg Ile Gly Arg Ile Leu Arg Leu Ile Arg Ala Ala Lys Gly Ile Arg
145 150 155 160
Thr Leu Leu Phe Ala Leu Met Met Ser Leu Pro Ala Leu Phe Asn Ile
165 170 175
Gly Leu Leu Leu Phe Leu Val Met Phe Ile Tyr Ser Ile Phe Gly Met
180 185 190
Ala Ser Phe Ala Asn Val Val Asp Glu Ala Gly Ile Asp Asp Met Phe
195 200 205
Asn Phe Lys Thr Phe Gly Asn Ser Met Leu Cys Leu Phe Gln Ile Thr
210 215 220
Thr Ser Ala Gly Trp Asp Gly Leu Leu Ser Pro Ile Leu Asn Thr Gly
225 230 235 240
Pro Pro Tyr Cys Asp Pro Asn Leu Pro Asn Ser Asn Gly Ser Arg Gly
245 250 255
Asn Cys Gly Ser Pro Ala Val Gly Ile Ile Phe Phe Thr Thr Tyr Ile
260 265 270
Ile Ile Ser Phe Leu Ile Val Val Asn Met Tyr Ile Ala Val Ile Leu
275 280 285

Glu Asn Phe Asn Val Ala Thr Glu Glu Ser Thr Glu Pro Leu Ser Glu
 290 295 300
 5 Asp Asp Phe Asp Met Phe Tyr Glu Thr Trp Glu Lys Phe Asp Pro Glu
 305 310 315 320
 Ala Thr Gln Phe Ile Ala Phe Ser Ala Leu Ser Asp Phe Ala Asp Thr
 325 330 335
 10 Leu Ser Gly Pro Leu Arg Ile Pro Lys Pro Asn Gln Asn Ile Leu Ile
 340 345 350
 Gln Met Asp Leu Pro Leu Val Pro Gly Asp Lys Ile His Cys Leu Asp
 355 360 365
 15 Ile Leu Phe Ala Phe Thr Lys Asn Val Leu Gly Glu Ser Gly Glu Leu
 370 375 380
 20 Asp Ser Leu Lys Thr Asn Met Glu Glu Lys Phe Met Ala Thr Asn Leu
 385 390 395 400
 Ser Lys Ala Ser Tyr Glu Pro Ile Ala Thr Thr Leu Arg Trp Lys Gln
 405 410 415
 25 Glu Asp Leu Ser Ala Thr Val Ile Gln Lys Ala Tyr Arg Ser Tyr Met
 420 425 430
 Leu His Arg Ser Leu Thr Leu Ser Asn Thr Leu His Val Pro Arg Ala
 435 440 445
 Glu Glu Asp Gly Val Ser Leu Pro Gly Glu Gly Tyr Ile Thr Phe Met
 450 455 460
 35 Ala Asn Ser Gly Leu Pro Asp Lys Ser Glu Thr Ala Ser Ala Thr Ser
 465 470 475 480
 Phe Pro Pro Ser Tyr Asp Ser Val Thr Arg Gly Leu Ser Asp Arg Ala
 485 490 495
 40 Asn Ile Asn Pro Ser Ser Ser Met Gln Asn Glu Asp Glu Val Ala Ala
 500 505 510
 Lys Glu Gly Asn Ser Pro Gly Pro Gln
 515 520
 45

(2) INFORMATION FOR SEQ ID NO:5:

50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 7052 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

55 (ii) MOLECULE TYPE: cDNA

60 (ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 204..6602

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

TAGCTTGCTT CTGCTAATGC TACCCCAGGC CTTTAGACAG AGAACAGATG GCAGATGGAG 60
 TTTCTTATTG CCATGCGCAA ACGCTGAGCC CACCTCATGA TCCCGGACCC CATGGTTTTC 120
 5 AGTAGACAAC CTGGGCTAAG AAGAGATCTC CGACCTTATA GAGCAGCAAA GAGTGTAAT 180
 TCTTCCCCAA GAAGAATGAG AAG ATG GAG CTC CCC TTT GCG TCC GTG GGA 230
 10 Met Glu Leu Pro Phe Ala Ser Val Gly
 1 5
 ACT ACC AAT TTC AGA CGG TTC ACT CCA GAG TCA CTG GCA GAG ATC GAG 278
 Thr Thr Asn Phe Arg Arg Phe Thr Pro Glu Ser Leu Ala Glu Ile Glu
 10 15
 AAG CAG ATT GCT GCT CAC CGG GCA GCC AAG AAG GCC AGA ACC AAG CAC 326
 Lys Gln Ile Ala Ala His Arg Ala Ala Lys Lys Ala Arg Thr Lys His
 30 40
 20 AGA GGA CAG GAG GAC AAG GGC GAG AAG CCC AGG CCT CAG CTG GAC TTG 374
 Arg Gly Gln Glu Asp Lys Gly Glu Lys Pro Arg Pro Gln Leu Asp Leu
 45 50 55
 AAA GAC TGT AAC CAG CTG CCC AAG TTC TAT GGT GAG CTC CCA GCA GAA 422
 25 Lys Asp Cys Asn Gln Leu Pro Lys Phe Tyr Gly Glu Leu Pro Ala Glu
 60 65 70
 CTG GTC GGG GAG CCC CTG GAG GAC CTA GAC CCT TTC TAC AGC ACA CAC 470
 30 Leu Val Gly Glu Pro Leu Glu Asp Leu Asp Pro Phe Tyr Ser Thr His
 75 80 85
 CGG ACA TTC ATG GTG TTG AAT AAA AGC AGG ACC ATT TCC AGA TTC AGT 518
 35 Arg Thr Phe Met Val Leu Asn Lys Ser Arg Thr Ile Ser Arg Phe Ser
 90 95 100 105
 GCC ACT TGG GCC CTG TGG CTC TTC AGT CCC TTC AAC CTG ATC AGA AGA 566
 Ala Thr Trp Ala Leu Trp Leu Phe Ser Pro Phe Asn Leu Ile Arg Arg
 110 115 120
 40 ACA GCC ATC AAA GTG TCT GTC CAT TCC TGG TTC TCC ATA TTC ATC ACC 614
 Thr Ala Ile Lys Val Ser Val His Ser Trp Phe Ser Ile Phe Ile Thr
 125 130 135
 ATC ACT ATT TTG GTC AAC TGC GTG TGC ATG ACC CGA ACT GAT CTT CCA 662
 45 Ile Thr Ile Leu Val Asn Cys Val Cys Met Thr Arg Thr Asp Leu Pro
 140 145 150
 GAG AAA GTC GAG TAC GTC TTC ACT GTC ATT TAC ACC TTC GAG GCT CTG 710
 50 Glu Lys Val Glu Tyr Val Phe Thr Val Ile Tyr Thr Phe Glu Ala Leu
 155 160 165
 ATT AAG ATA CTG GCA AGA GGG TTT TGT CTA AAT GAG TTC ACT TAT CTT 758
 55 Ile Lys Ile Leu Ala Arg Gly Phe Cys Leu Asn Glu Phe Thr Tyr Leu
 170 175 180 185
 CGA GAT CCG TGG AAC TGG CTG GAC TTC AGT GTC ATT ACC TTG GCG TAT 806
 Arg Asp Pro Trp Asn Trp Leu Asp Phe Ser Val Ile Thr Leu Ala Tyr
 190 195 200
 60 GTG GGT GCA GCG ATA GAC CTC CGA GGA ATC TCA GGC CTG CGG ACA TTC 854
 Val Gly Ala Ala Ile Asp Leu Arg Gly Ile Ser Gly Leu Arg Thr Phe
 205 210 215

	CGA	GTT	CTC	AGA	GCC	CTG	AAA	ACT	GTT	TCT	GTG	ATC	CCA	GGA	CTG	AAG	902
	Arg	Val	Leu	Arg	Ala	Leu	Lys	Thr	Val	Ser	Val	Ile	Pro	Gly	Leu	Lys	
			220					225					230				
5	GTC	ATC	GTG	GGA	GCC	CTG	ATC	CAC	TCA	GTG	AGG	AAG	CTG	GCC	GAC	GTG	950
	Val	Ile	Val	Gly	Ala	Leu	Ile	His	Ser	Val	Arg	Lys	Leu	Ala	Asp	Val	
			235				240					245					
10	ACT	ATC	CTC	ACA	GTC	TTC	TGC	CTG	AGC	GTC	TTC	GCC	TTG	GTG	GGC	CTG	998
	Thr	Ile	Leu	Thr	Val	Phe	Cys	Leu	Ser	Val	Phe	Ala	Leu	Val	Gly	Leu	
			250			255					260					265	
15	CAG	CTC	TTT	AAG	GGG	AAC	CTT	AAG	AAC	AAA	TGC	ATC	AGG	AAC	GGA	ACA	1046
	Gln	Leu	Phe	Lys	Gly	Asn	Leu	Lys	Asn	Lys	Cys	Ile	Arg	Asn	Gly	Thr	
					270					275					280		
	GAT	CCC	CAC	AAG	GCT	GAC	AAC	CTC	TCA	TCT	GAA	ATG	GCA	GAA	TAC	ATC	1094
	Asp	Pro	His	Lys	Ala	Asp	Asn	Leu	Ser	Ser	Glu	Met	Ala	Glu	Tyr	Ile	
				285					290					295			
20	TTC	ATC	AAG	CCT	GGT	ACT	ACG	GAT	CCC	TTA	CTG	TGC	GGC	AAT	GGG	TCT	1142
	Phe	Ile	Lys	Pro	Gly	Thr	Thr	Asp	Pro	Leu	Leu	Cys	Gly	Asn	Gly	Ser	
			300					305					310				
25	GAT	GCT	GGT	CAC	TGC	CCT	GGA	GGC	TAT	GTC	TGC	CTG	AAA	ACT	CCT	GAC	1190
	Asp	Ala	Gly	His	Cys	Pro	Gly	Gly	Tyr	Val	Cys	Leu	Lys	Thr	Pro	Asp	
			315				320					325					
30	AAC	CCG	GAT	TTT	AAC	TAC	ACC	AGC	TTT	GAT	TCC	TTT	GCG	TGG	GCA	TTC	1238
	Asn	Pro	Asp	Phe	Asn	Tyr	Thr	Ser	Phe	Asp	Ser	Phe	Ala	Trp	Ala	Phe	
						335					340					345	
35	CTC	TCA	CTG	TTC	CGC	CTC	ATG	ACG	CAG	GAC	TCC	TGG	GAG	CGC	CTG	TAC	1286
	Leu	Ser	Leu	Phe	Arg	Leu	Met	Thr	Gln	Asp	Ser	Trp	Glu	Arg	Leu	Tyr	
					350					355					360		
	CAG	CAG	ACA	CTC	CGG	GCT	TCT	GGG	AAA	ATG	TAC	ATG	GTC	TTT	TTC	GTG	1334
	Gln	Gln	Thr	Leu	Arg	Ala	Ser	Gly	Lys	Met	Tyr	Met	Val	Phe	Phe	Val	
				365					370					375			
40	CTG	GTT	ATT	TTC	CTT	GGA	TCG	TTC	TAC	CTG	GTC	AAT	TTG	ATC	TTG	GCC	1382
	Leu	Val	Ile	Phe	Leu	Gly	Ser	Phe	Tyr	Leu	Val	Asn	Leu	Ile	Leu	Ala	
			380					385					390				
45	GTG	GTC	ACC	ATG	GCG	TAT	GAA	GAG	CAG	AGC	CAG	GCA	ACA	ATT	GCA	GAA	1430
	Val	Val	Thr	Met	Ala	Tyr	Glu	Glu	Gln	Ser	Gln	Ala	Thr	Ile	Ala	Glu	
			395				400					405					
50	ATC	GAA	GCC	AAG	GAA	AAA	AAG	TTC	CAG	GAA	GCC	CTT	GAG	GTG	CTG	CAG	1478
	Ile	Glu	Ala	Lys	Glu	Lys	Lys	Phe	Gln	Glu	Ala	Leu	Glu	Val	Leu	Gln	
			410			415					420					425	
55	AAG	GAA	CAG	GAG	GTG	CTG	GCA	GCC	CTG	GGG	ATT	GAC	ACG	ACC	TCG	CTC	1526
	Lys	Glu	Gln	Glu	Val	Leu	Ala	Ala	Leu	Gly	Ile	Asp	Thr	Thr	Ser	Leu	
					430					435					440		
	CAG	TCC	CAC	AGT	GGA	TCA	CCC	TTA	GCC	TCC	AAA	AAC	GCC	AAT	GAG	AGA	1574
	Gln	Ser	His	Ser	Gly	Ser	Pro	Leu	Ala	Ser	Lys	Asn	Ala	Asn	Glu	Arg	
				445					450				455				
60	AGA	CCC	AGG	GTG	AAA	TCA	AGG	GTG	TCA	GAG	GGC	TCC	ACG	GAT	GAC	AAC	1622
	Arg	Pro	Arg	Val	Lys	Ser	Arg	Val	Ser	Glu	Gly	Ser	Thr	Asp	Asp	Asn	
			460				465						470				

AGG TCA CCC CAA TCT GAC CCT TAC AAC CAG CGC AGG ATG TCT TTC CTA 1670
 Arg Ser Pro Gln Ser Asp Pro Tyr Asn Gln Arg Arg Met Ser Phe Leu
 475 480 485

5 GGC CTG TCT TCA GGA AGA CGC AGG GCT AGC CAC GGC AGT GTG TTC CAC 1718
 Gly Leu Ser Ser Gly Arg Arg Arg Ala Ser His Gly Ser Val Phe His
 490 495 500 505

10 TTC CGA GCG CCC AGC CAA GAC ATC TCA TTT CCT GAC GGG ATC ACC CCT 1766
 Phe Arg Ala Pro Ser Gln Asp Ile Ser Phe Pro Asp Gly Ile Thr Pro
 510 515 520

15 GAT GAT GGG GTC TTT CAC GGA GAC CAG GAA AGC CGT CGA GGT TCC ATA 1814
 Asp Asp Gly Val Phe His Gly Asp Gln Glu Ser Arg Arg Gly Ser Ile
 525 530 535

20 TTG CTG GGC AGG GGT GCT GGG CAG ACA GGT CCA CTC CCC AGG AGC CCA 1862
 Leu Leu Gly Arg Gly Ala Gly Gln Thr Gly Pro Leu Pro Arg Ser Pro
 540 545 550

CTG CCT CAG TCC CCC AAC GCT GGC CGT AGA CAT GGA GAA GAG GGA CAG 1910
 Leu Pro Gln Ser Pro Asn Pro Gly Arg Arg His Gly Glu Glu Gly Gln
 555 560 565

25 CTC GGA GTG CCC ACT GGT GAG CTT ACC GCT GGA GCG CCT GAA GGC CCG 1958
 Leu Gly Val Pro Thr Gly Glu Leu Thr Ala Gly Ala Pro Glu Gly Pro
 570 575 580 585

30 GCA CTC GAC ACT ACA GGG CAG AAG AGC TTC CTG TCT GCG GGC TAC TTG 2006
 Ala Leu Asp Thr Thr Gly Gln Lys Ser Phe Leu Ser Ala Gly Tyr Leu
 590 595 600

35 AAC GAA CCT TTC CGA GCA CAG AGG GCC ATG AGC GTT GTC AGT ATC ATG 2054
 Asn Glu Pro Phe Arg Ala Gln Arg Ala Met Ser Val Val Ser Ile Met
 605 610 615

40 ACT TCT GTC ATT GAG GAG CTT GAA GAG TCT AAG CTG AAG TGC CCA CCC 2102
 Thr Ser Val Ile Glu Glu Leu Glu Glu Ser Lys Leu Lys Cys Pro Pro
 620 625 630

TGC TTG ATC AGC TTC GCT CAG AAG TAT CTG ATC TGG GAG TGC TGC CCC 2150
 Cys Leu Ile Ser Phe Ala Gln Lys Tyr Leu Ile Trp Glu Cys Cys Pro
 635 640 645

45 AAG TGG AGG AAG TTC AAG ATG GCG CTG TTC GAG CTG GTG ACT GAC CCC 2198
 Lys Trp Arg Lys Phe Lys Met Ala Leu Phe Glu Leu Val Thr Asp Pro
 650 655 660 665

50 TTC GCA GAG CTT ACC ATC ACC CTC TGC ATC GTG GTG AAC ACC GTC TTC 2246
 Phe Ala Glu Leu Thr Ile Thr Leu Cys Ile Val Val Asn Thr Val Phe
 670 675 680

55 ATG GCC ATG GAG CAC TAC CCC ATG ACC GAT GCC TTC GAT GCC ATG CTT 2294
 Met Ala Met Glu His Tyr Pro Met Thr Asp Ala Phe Asp Ala Met Leu
 685 690 695

60 CAA GCC GGC AAC ATT GTC TTC ACC GTG TTT TTC ACA ATG GAG ATG GCC 2342
 Gln Ala Gly Asn Ile Val Phe Thr Val Phe Phe Thr Met Glu Met Ala
 700 705 710

TTC AAG ATC ATT GCC TTC GAC CCC TAC TAT TAC TTC CAG AAG AAG TGG 2390
 Phe Lys Ile Ile Ala Phe Asp Pro Tyr Tyr Tyr Phe Gln Lys Lys Trp
 715 720 725

	AAT	ATC	TTC	GAC	TGT	GTC	ATC	GTC	ACC	GTG	AGC	CTT	CTG	GAG	CTG	AGT	2438
	Asn	Ile	Phe	Asp	Cys	Val	Ile	Val	Thr	Val	Ser	Leu	Leu	Glu	Leu	Ser	
	730					735					740					745	
5	GCA	TCC	AAG	AAG	GGC	AGC	CTG	TCT	GTG	CTC	CGT	TCC	TTA	CGC	TTG	GCA	2486
	Ala	Ser	Lys	Lys	Gly	Ser	Leu	Ser	Val	Leu	Arg	Ser	Leu	Arg	Leu	Ala	
					750					755					760		
10	CTC	GAC	ACT	ACA	GGG	CAG	AAG	AGC	TTC	CTG	TCT	GCG	GGC	TAC	TTG	AAC	2534
	Leu	Asp	Thr	Thr	Gly	Gln	Lys	Ser	Phe	Leu	Ser	Ala	Gly	Tyr	Leu	Asn	
				765					770					775			
15	GAA	CCT	TTC	CGA	GCA	CAG	AGG	GCC	ATG	AGC	GTT	GTC	AGT	ATC	ATG	ACT	2582
	Glu	Pro	Phe	Arg	Ala	Gln	Arg	Ala	Met	Ser	Val	Val	Ser	Ile	Met	Thr	
			780					785					790				
20	TCT	GTC	ATT	GAG	GAG	CTT	GAA	GAG	TCT	AAG	CTG	AAG	TGC	CCA	CCC	TGC	2630
	Ser	Val	Ile	Glu	Glu	Leu	Glu	Glu	Ser	Lys	Leu	Lys	Cys	Pro	Pro	Cys	
		795				800						805					
25	TTG	ATC	AGC	TTC	GCT	CAG	AAG	TAT	CTG	ATC	TGG	GAG	TGC	TGC	CCC	AAG	2678
	Leu	Ile	Ser	Phe	Ala	Gln	Lys	Tyr	Leu	Ile	Trp	Glu	Cys	Cys	Pro	Lys	
	810					815					820					825	
30	TGG	AGG	AAG	TTC	AAG	ATG	GCG	CTG	TTC	GAG	CTG	GTG	ACT	GAC	CCC	TTC	2726
	Trp	Arg	Lys	Phe	Lys	Met	Ala	Leu	Phe	Glu	Leu	Val	Thr	Asp	Pro	Phe	
					830					835					840		
35	GCA	GAG	CTT	ACC	ATC	ACC	CTC	TGC	ATC	GTG	GTG	AAC	ACC	GTC	TTC	ATG	2774
	Ala	Glu	Leu	Thr	Ile	Thr	Leu	Cys	Ile	Val	Val	Asn	Thr	Val	Phe	Met	
				845				850						855			
40	GCC	ATG	GAG	CAC	TAC	CCC	ATG	ACC	GAT	GCC	TTC	GAT	GCC	ATG	CTT	CAA	2822
	Ala	Met	Glu	His	Tyr	Pro	Met	Thr	Asp	Ala	Phe	Asp	Ala	Met	Leu	Gln	
			860					865					870				
45	GCC	GGC	AAC	ATT	GTC	TTC	ACC	GTG	TTT	TTC	ACA	ATG	GAG	ATG	GCC	TTC	2870
	Ala	Gly	Asn	Ile	Val	Phe	Thr	Val	Phe	Phe	Thr	Met	Glu	Met	Ala	Phe	
		875					880					885					
50	AAG	ATC	ATT	GCC	TTC	GAC	CCC	TAC	TAT	TAC	TTC	CAG	AAG	AAG	TGG	AAT	2918
	Lys	Ile	Ile	Ala	Phe	Asp	Pro	Tyr	Tyr	Tyr	Phe	Gln	Lys	Lys	Trp	Asn	
	890					895					900					905	
55	ATC	TTC	GAC	TGT	GTC	ATC	GTC	ACC	GTG	AGC	CTT	CTG	GAG	CTG	AGT	GCA	2966
	Ile	Phe	Asp	Cys	Val	Ile	Val	Thr	Val	Ser	Leu	Leu	Glu	Leu	Ser	Ala	
					910					915					920		
60	TCC	AAG	AAG	GGC	AGC	CTG	TCT	GTG	CTC	CGT	TCC	TTA	CGC	TTG	CTG	CGG	3014
	Ser	Lys	Lys	Gly	Ser	Leu	Ser	Val	Leu	Arg	Ser	Leu	Arg	Leu	Leu	Arg	
				925					930					935			
65	GTC	TTC	AAG	CTG	GCC	AAG	TCC	TGG	CCC	ACC	CTG	AAC	ACC	CTC	ATC	AAG	3062
	Val	Phe	Lys	Leu	Ala	Lys	Ser	Trp	Pro	Thr	Leu	Asn	Thr	Leu	Ile	Lys	
			940					945					950				
70	ATC	ATC	GGG	AAC	TCA	GTG	GGG	GCC	CTG	GGC	AAC	CTG	ACC	TTT	ATC	CTG	3110
	Ile	Ile	Gly	Asn	Ser	Val	Gly	Ala	Leu	Gly	Asn	Leu	Thr	Phe	Ile	Leu	
		955					960					965					
75	GCC	ATC	ATC	GTC	TTC	ATC	TTC	GCC	CTG	GTC	GGA	AAG	CAG	CTT	CTC	TCA	3158
	Ala	Ile	Ile	Val	Phe	Ile	Phe	Ala	Leu	Val	Gly	Lys	Gln	Leu	Leu	Ser	
	970					975					980					985	

GAG GAC TAC GGG TGC CGC AAG GAC GGC GTC TCC GTG TGG AAC GGC GAG 3206
 Glu Asp Tyr Gly Cys Arg Lys Asp Gly Val Ser Val Trp Asn Gly Glu
 990 995 1000

5 AAG CTC CGC TGG CAC ATG TGT GAC TTC TTC CAT TCC TTC CTG GTC GTC 3254
 Lys Leu Arg Trp His Met Cys Asp Phe Phe His Ser Phe Leu Val Val
 1005 1010 1015

10 TTC CGA ATC CTC TGC GGG GAG TGG ATC GAG AAC ATG TGG GTC TGC ATG 3302
 Phe Arg Ile Leu Cys Gly Glu Trp Ile Glu Asn Met Trp Val Cys Met
 1020 1025 1030

15 GAG GTC AGC CAG AAA TCC ATC TGC CTC ATC CTC TTC TTG ACT GTG ATG 3350
 Glu Val Ser Gln Lys Ser Ile Cys Leu Ile Leu Phe Leu Thr Val Met
 1035 1040 1045

20 GTG CTG GGC AAC CTA GTG GTG CTC AAC CTT TTC ATC GCT TTA CTG CTG 3398
 Val Leu Gly Asn Leu Val Val Leu Asn Leu Phe Ile Ala Leu Leu Leu
 1050 1055 1060 1065

AAC TCC TTC AGC GCG GAC AAC CTC ACG GCT CCA GAG GAT GAC GGG GAG 3446
 Asn Ser Phe Ser Ala Asp Asn Leu Thr Ala Pro Glu Asp Asp Gly Glu
 1070 1075 1080

25 GTG AAC AAC TTG CAG TTA GCA CTG GCC AGG ATC CAG GTA CTT GGC CAT 3494
 Val Asn Asn Leu Gln Leu Ala Leu Ala Arg Ile Gln Val Leu Gly His
 1085 1090 1095

30 CGG GCC AGC AGG GCC ATC GCC AGT TAC ATC AGC AGC CAC TGC CGA TTC 3542
 Arg Ala Ser Arg Ala Ile Ala Ser Tyr Ile Ser Ser His Cys Arg Phe
 1100 1105 1110

35 CGC TGG CCC AAG GTG GAG ACC CAG CTG GGC ATG AAG CCC CCA CTC ACC 3590
 Arg Trp Pro Lys Val Glu Thr Gln Leu Gly Met Lys Pro Pro Leu Thr
 1115 1120 1125

40 AGC TCA GAG GCC AAG AAC CAC ATT CCC ACT GAT GCT GTC AGT GCT GCA 3638
 Ser Ser Glu Ala Lys Asn His Ile Ala Thr Asp Ala Val Ser Ala Ala
 1130 1135 1140 1145

GTG GGG AAC CTG ACA AAG CCA GCT CTC AGT AGC CCC AAG GAG AAT CAC 3686
 Val Gly Asn Leu Thr Lys Pro Ala Leu Ser Ser Pro Lys Glu Asn His
 1150 1155 1160

45 GGG GAC TTC ATC ACT GAT CCC AAC GTG TGG GTC TCT GTG CCC ATT GCT 3734
 Gly Asp Phe Ile Thr Asp Pro Asn Val Trp Val Ser Val Pro Ile Ala
 1165 1170 1175

50 GAG GGG GAA TCT GAC CTC GAC GAG CTC GAG GAA GAT ATG GAG CAG GCT 3782
 Glu Gly Glu Ser Asp Leu Asp Glu Leu Glu Glu Asp Met Glu Gln Ala
 1180 1185 1190

55 TCG CAG AGC TCC TGG CAG GAA GAG GAC CCC AAG GGA CAG CAG GAG CAG 3830
 Ser Gln Ser Ser Trp Gln Glu Glu Asp Pro Lys Gly Gln Gln Glu Gln
 1195 1200 1205

TTG CCA CAA GTC CAA AAG TGT GAA AAC CAC CAG GCA GCC AGA AGC CCA 3878
 Leu Pro Gln Val Gln Lys Cys Glu Asn His Gln Ala Ala Arg Ser Pro
 1210 1215 1220 1225

60 GCC TCC ATG ATG TCC TCT GAG GAC CTG GCT CCA TAC CTG GGT GAG AGC 3926
 Ala Ser Met Met Ser Ser Glu Asp Leu Ala Pro Tyr Leu Gly Glu Ser
 1230 1235 1240

	TGG	AAG	AGG	AAG	GAT	AGC	CCT	CAG	GTC	CCT	GCC	GAG	GGA	GTG	GAT	GAC	3974
	Trp	Lys	Arg	Lys	Asp	Ser	Pro	Gln	Val	Pro	Ala	Glu	Gly	Val	Asp	Asp	
				1245					1250					1255			
5	ACG	AGC	TCC	TCT	GAG	GGC	AGC	ACG	GTG	GAC	TGC	CCG	GAC	CCA	GAG	GAA	4022
	Thr	Ser	Ser	Ser	Glu	Gly	Ser	Thr	Val	Asp	Cys	Pro	Asp	Pro	Glu	Glu	
			1260					1265					1270				
10	ATC	CTG	AGG	AAG	ATC	CCC	GAG	CTG	GCA	GAT	GAC	CTG	GAC	GAG	CCC	GAT	4070
	Ile	Leu	Arg	Lys	Ile	Pro	Glu	Leu	Ala	Asp	Asp	Leu	Asp	Glu	Pro	Asp	
			1275				1280					1285					
15	GAC	TGT	TTC	ACA	GAA	GGC	TGC	ACT	CGC	CGC	TGT	CCC	TGC	TGC	AAC	GTG	4118
	Asp	Cys	Phe	Thr	Glu	Gly	Cys	Thr	Arg	Arg	Cys	Pro	Cys	Cys	Asn	Val	
			1290			1295					1300					1305	
20	AAT	ACT	AGC	AAG	TCT	CCT	TGG	GCC	ACA	GGC	TGG	CAG	GTG	CGC	AAG	ACC	4166
	Asn	Thr	Ser	Lys	Ser	Pro	Trp	Ala	Thr	Gly	Trp	Gln	Val	Arg	Lys	Thr	
				1310						1315					1320		
25	TGC	TAC	CGC	ATC	GTG	GAG	CAC	AGC	TGG	TTT	GAG	AGT	TTC	ATC	ATC	TTC	4214
	Cys	Tyr	Arg	Ile	Val	Glu	His	Ser	Trp	Phe	Glu	Ser	Phe	Ile	Ile	Phe	
				1325					1330					1335			
30	ATG	ATC	CTG	CTC	AGC	AGT	GGA	GCG	CTG	GCC	TTT	GAG	GAT	AAC	TAC	CTG	4262
	Met	Ile	Leu	Leu	Ser	Ser	Gly	Ala	Leu	Ala	Phe	Glu	Asp	Asn	Tyr	Leu	
			1340				1345					1350					
35	GAA	GAG	AAA	CCC	CGA	GTG	AAG	TCC	GTG	CTG	GAG	TAC	ACT	GAC	CGA	GTG	4310
	Glu	Glu	Lys	Pro	Arg	Val	Lys	Ser	Val	Leu	Glu	Tyr	Thr	Asp	Arg	Val	
			1355				1360					1365					
40	TTC	ACC	TTC	ATC	TTC	GTC	TTT	GAG	ATG	CTG	CTC	AAG	TGG	GTA	GCC	TAT	4358
	Phe	Thr	Phe	Ile	Phe	Val	Phe	Glu	Met	Leu	Leu	Lys	Trp	Val	Ala	Tyr	
			1370			1375					1380					1385	
45	GGC	TTC	AAA	AAG	TAT	TTC	ACC	AAT	GCC	TGG	TGC	TGG	CTG	GAC	TTC	CTC	4406
	Gly	Phe	Lys	Lys	Tyr	Phe	Thr	Asn	Ala	Trp	Cys	Trp	Leu	Asp	Phe	Leu	
				1390					1395					1400			
50	ATT	GTG	AAC	ATC	TCC	CTG	ACA	AGC	CTC	ATA	GCG	AAG	ATC	CTT	GAG	TAT	4454
	Ile	Val	Asn	Ile	Ser	Leu	Thr	Ser	Leu	Ile	Ala	Lys	Ile	Leu	Glu	Tyr	
				1405					1410				1415				
55	TCC	GAC	GTG	GCG	TCC	ATC	AAA	GCC	CTT	CGG	ACT	CTC	CGT	GCC	CTC	CGA	4502
	Ser	Asp	Val	Ala	Ser	Ile	Lys	Ala	Leu	Arg	Thr	Leu	Arg	Ala	Leu	Arg	
			1420				1425					1430					
60	CCG	CTG	CGG	GCT	CTG	TCT	CGA	TTC	GAA	GGC	ATG	AGG	GTA	GTC	GTG	GAT	4550
	Pro	Leu	Arg	Ala	Leu	Ser	Arg	Phe	Glu	Gly	Met	Arg	Val	Val	Val	Asp	
			1435				1440					1445					
65	GCC	CTC	GTG	GGC	GCC	ATC	CCC	TCC	ATC	ATG	AAC	GTC	CTC	CTC	GTC	TGC	4598
	Ala	Leu	Val	Gly	Ala	Ile	Pro	Ser	Ile	Met	Asn	Val	Leu	Leu	Val	Cys	
			1450			1455					1460					1465	
70	CTC	ATC	TTC	TGG	CTC	ATC	TTC	AGC	ATC	ATG	GGC	GTG	AAC	CTC	TTC	GCC	4646
	Leu	Ile	Phe	Trp	Leu	Ile	Phe	Ser	Ile	Met	Gly	Val	Asn	Leu	Phe	Ala	
				1470						1475				1480			
75	GGG	AAA	TTT	TCG	AAG	TGC	GTC	GAC	ACC	AGA	AAT	AAC	CCA	TTT	TCC	AAC	4694
	Gly	Lys	Phe	Ser	Lys	Cys	Val	Asp	Thr	Arg	Asn	Asn	Pro	Phe	Ser	Asn	
				1485				1490						1495			

	GTG	AAT	TCG	ACG	ATG	GTG	AAT	AAC	AAG	TCC	GAG	TGT	CAC	AAT	CAA	AAC	4742
	Val	Asn	Ser	Thr	Met	Val	Asn	Asn	Lys	Ser	Glu	Cys	His	Asn	Gln	Asn	
			1500					1505					1510				
5	AGC	ACC	GGC	CAC	TTC	TTC	TGG	GTC	AAC	GTC	AAA	GTC	AAC	TTC	GAC	AAC	4790
	Ser	Thr	Gly	His	Phe	Phe	Trp	Val	Asn	Val	Lys	Val	Asn	Phe	Asp	Asn	
			1515				1520					1525					
10	GTC	GCT	ATG	GGC	TAC	CTC	GCA	CTT	CTT	CAG	GTG	GCA	ACC	TTC	AAA	GGC	4838
	Val	Ala	Met	Gly	Tyr	Leu	Ala	Leu	Leu	Gln	Val	Ala	Thr	Phe	Lys	Gly	
			1530			1535					1540					1545	
15	TGG	ATG	GAC	ATA	ATG	TAT	GCA	GCT	GTT	GAT	TCC	GGA	GAG	ATC	AAC	AGT	4886
	Trp	Met	Asp	Ile	Met	Tyr	Ala	Ala	Val	Asp	Ser	Gly	Glu	Ile	Asn	Ser	
					1550					1555					1560		
20	CAG	CCT	AAC	TGG	GAG	AAC	AAC	TTG	TAC	ATG	TAC	CTG	TAC	TTC	GTC	GTT	4934
	Gln	Pro	Asn	Trp	Glu	Asn	Asn	Leu	Tyr	Met	Tyr	Leu	Tyr	Phe	Val	Val	
				1565				1570						1575			
	TTC	ATC	ATT	TTC	GGT	GGC	TTC	TTC	ACG	CTG	AAT	CTC	TTT	GTT	GGG	GTC	4982
	Phe	Ile	Ile	Phe	Gly	Gly	Phe	Phe	Thr	Leu	Asn	Leu	Phe	Val	Gly	Val	
				1580				1585					1590				
25	ATA	ATC	GAC	AAC	TTC	AAC	CAA	CAG	AAA	AAA	AAG	CTA	GGA	GGC	CAG	GAC	5030
	Ile	Ile	Asp	Asn	Phe	Asn	Gln	Gln	Lys	Lys	Lys	Leu	Gly	Gly	Gln	Asp	
			1595				1600					1605					
30	ATC	TTC	ATG	ACA	GAA	GAG	CAG	AAG	AAG	TAC	TAC	AAT	GCC	ATG	AAG	AAG	5078
	Ile	Phe	Met	Thr	Glu	Glu	Gln	Lys	Lys	Tyr	Tyr	Asn	Ala	Met	Lys	Lys	
					1610		1615				1620					1625	
35	CTG	GGC	TCC	AAG	AAA	CCC	CAG	AAG	CCC	ATC	CCA	CGG	CCC	CTG	AAT	AAG	5126
	Leu	Gly	Ser	Lys	Lys	Pro	Gln	Lys	Pro	Ile	Pro	Arg	Pro	Leu	Asn	Lys	
					1630					1635					1640		
40	TAC	CAA	GGC	TTC	GTG	TTT	GAC	ATC	GTG	ACC	AGG	CAA	GCC	TTT	GAC	ATC	5174
	Tyr	Gln	Gly	Phe	Val	Phe	Asp	Ile	Val	Thr	Arg	Gln	Ala	Phe	Asp	Ile	
				1645					1650					1655			
	ATC	ATC	ATG	GTT	CTC	ATC	TGC	CTC	AAC	ATG	ATC	ACC	ATG	ATG	GTG	GAG	5222
	Ile	Ile	Met	Val	Leu	Ile	Cys	Leu	Asn	Met	Ile	Thr	Met	Met	Val	Glu	
				1660				1665					1670				
45	ACC	GAC	GAG	CAG	GGC	GAG	GAG	AAG	ACG	AAG	GTT	CTG	GGC	AGA	ATC	AAC	5270
	Thr	Asp	Glu	Gln	Gly	Glu	Glu	Lys	Thr	Lys	Val	Leu	Gly	Arg	Ile	Asn	
			1675				1680					1685					
50	CAG	TTC	TTT	GTG	GCC	GTC	TTC	ACG	GGC	GAG	TGT	GTG	ATG	AAG	ATG	TTC	5318
	Gln	Phe	Phe	Val	Ala	Val	Phe	Thr	Gly	Glu	Cys	Val	Met	Lys	Met	Phe	
				1690		1695					1700					1705	
55	GCC	CTG	CGA	CAG	TAC	TAC	TTC	ACC	AAC	GGC	TGG	AAC	GTG	TTC	GAC	TTC	5366
	Ala	Leu	Arg	Gln	Tyr	Tyr	Phe	Thr	Asn	Gly	Trp	Asn	Val	Phe	Asp	Phe	
					1710					1715					1720		
60	ATA	GTG	GTG	ATC	CTG	TCC	ATT	GGG	AGT	CTG	CTG	TTT	TCT	GCA	ATC	CTT	5414
	Ile	Val	Val	Ile	Leu	Ser	Ile	Gly	Ser	Leu	Leu	Phe	Ser	Ala	Ile	Leu	
				1725				1730						1735			
	AAG	TCA	CTG	GAA	AAC	TAC	TTC	TCC	CCG	ACG	CTC	TTC	CGG	GTC	ATC	CGT	5462
	Lys	Ser	Leu	Glu	Asn	Tyr	Phe	Ser	Pro	Thr	Leu	Phe	Arg	Val	Ile	Arg	
			1740					1745					1750				

	CTG	GCC	AGG	ATC	GGC	CGC	ATC	CTC	AGG	CTG	ATC	CGA	GCA	GCC	AAG	GGG	5510
	Leu	Ala	Arg	Ile	Gly	Arg	Ile	Leu	Arg	Leu	Ile	Arg	Ala	Ala	Lys	Gly	
		1755					1760					1765					
5	ATT	CGC	ACG	CTG	CTC	TTC	GCC	CTC	ATG	ATG	TCC	CTG	CCC	GCC	CTC	TTC	5558
	Ile	Arg	Thr	Leu	Leu	Phe	Ala	Leu	Met	Met	Ser	Leu	Pro	Ala	Leu	Phe	
	1770					1775					1780					1785	
10	AAC	ATC	GGC	CTC	CTC	CTC	TTC	CTC	GTC	ATG	TTC	ATC	TAC	TCC	ATC	TTC	5606
	Asn	Ile	Gly	Leu	Leu	Leu	Phe	Leu	Val	Met	Phe	Ile	Tyr	Ser	Ile	Phe	
					1790					1795					1800		
15	GGC	ATG	GCC	AGC	TTC	GCT	AAC	GTC	GTG	GAC	GAG	GCC	GGC	ATC	GAC	GAC	5654
	Gly	Met	Ala	Ser	Phe	Ala	Asn	Val	Val	Asp	Glu	Ala	Gly	Ile	Asp	Asp	
				1805					1810					1815			
20	ATG	TTC	AAC	TTC	AAG	ACC	TTT	GGC	AAC	AGC	ATG	CTG	TGC	CTG	TTC	CAG	5702
	Met	Phe	Asn	Phe	Lys	Thr	Phe	Gly	Asn	Ser	Met	Leu	Cys	Leu	Phe	Gln	
			1820					1825					1830				
25	ATC	ACC	ACC	TCG	GCC	GGC	TGG	GAC	GGC	CTC	CTC	AGC	CCC	ATC	CTC	AAC	5750
	Ile	Thr	Thr	Ser	Ala	Gly	Trp	Asp	Gly	Leu	Leu	Ser	Pro	Ile	Leu	Asn	
	1835						1840						1845				
30	ACG	GGG	CCT	CCC	TAC	TGC	GAC	CCC	AAC	CTG	CCC	AAC	AGC	AAC	GGC	TCC	5798
	Thr	Gly	Pro	Pro	Tyr	Cys	Asp	Pro	Asn	Leu	Pro	Asn	Ser	Asn	Gly	Ser	
	1850					1855				1860						1865	
35	CGG	GGG	AAC	TGC	GGG	AGC	CCG	GCG	GTG	GGC	ATC	ATC	TTC	TTC	ACC	ACC	5846
	Arg	Gly	Asn	Cys	Gly	Ser	Pro	Ala	Val	Gly	Ile	Ile	Phe	Phe	Thr	Thr	
				1870						1875					1880		
40	TAC	ATC	ATC	ATC	TCC	TTC	CTC	ATC	GTG	GTC	AAC	ATG	TAC	ATC	GCA	GTG	5894
	Tyr	Ile	Ile	Ile	Ser	Phe	Leu	Ile	Val	Val	Asn	Met	Tyr	Ile	Ala	Val	
				1885					1890					1895			
45	ATT	CTG	GAG	AAC	TTC	AAC	GTA	GCC	ACC	GAG	GAG	AGC	ACG	GAG	CCC	CTG	5942
	Ile	Leu	Glu	Asn	Phe	Asn	Val	Ala	Thr	Glu	Glu	Ser	Thr	Glu	Pro	Leu	
		1900					1905						1910				
50	AGC	GAG	GAC	GAC	TTC	GAC	ATG	TTC	TAT	GAG	ACC	TGG	GAG	AAG	TTC	GAC	5990
	Ser	Glu	Asp	Asp	Phe	Asp	Met	Phe	Tyr	Glu	Thr	Trp	Glu	Lys	Phe	Asp	
		1915					1920					1925					
55	CCG	GAG	GCC	ACC	CAG	TTC	ATT	GCC	TTT	TCT	GCC	CTC	TCA	GAC	TTC	GCG	6038
	Pro	Glu	Ala	Thr	Gln	Phe	Ile	Ala	Phe	Ser	Ala	Leu	Ser	Asp	Phe	Ala	
	1930				1935					1940						1945	
60	GAC	ACG	CTC	TCC	GGC	CCT	CTT	AGA	ATC	CCC	AAA	CCC	AAC	CAG	AAT	ATA	6086
	Asp	Thr	Leu	Ser	Gly	Pro	Leu	Arg	Ile	Pro	Lys	Pro	Asn	Gln	Asn	Ile	
				1950					1955					1960			
65	TTA	ATC	CAG	ATG	GAC	CTG	CCG	TTG	GTC	CCC	GGG	GAT	AAG	ATC	CAC	TGT	6134
	Leu	Ile	Gln	Met	Asp	Leu	Pro	Leu	Val	Pro	Gly	Asp	Lys	Ile	His	Cys	
			1965					1970						1975			
70	CTG	GAC	ATC	CTT	TTT	GCC	TTC	ACA	AAG	AAC	GTC	TTG	GGA	GAA	TCC	GGG	6182
	Leu	Asp	Ile	Leu	Phe	Ala	Phe	Thr	Lys	Asn	Val	Leu	Gly	Glu	Ser	Gly	
		1980					1985						1990				
75	GAG	TTG	GAC	TCC	CTG	AAG	ACC	AAT	ATG	GAA	GAG	AAG	TTT	ATG	GCG	ACC	6230
	Glu	Leu	Asp	Ser	Leu	Lys	Thr	Asn	Met	Glu	Glu	Lys	Phe	Met	Ala	Thr	
	1995						2000					2005					

AAT CTC TCC AAA GCA TCC TAT GAA CCA ATA GCC ACC ACC CTC CGG TGG 6278
Asn Leu Ser Lys Ala Ser Tyr Glu Pro Ile Ala Thr Thr Leu Arg Trp
2010 2015 2020 2025

5 AAG CAG GAA GAC CTC TCA GCC ACA GTC ATT CAA AAG GCC TAC CGG AGC 6326
Lys Gln Glu Asp Leu Ser Ala Thr Val Ile Gln Lys Ala Tyr Arg Ser
2030 2035 2040

10 TAC ATG CTG CAC CGC TCC TTG ACA CTC TCC AAC ACC CTG CAT GTG CCC 6374
Tyr Met Leu His Arg Ser Leu Thr Leu Ser Asn Thr Leu His Val Pro
2045 2050 2055

15 AGG GCT GAG GAG GAT GGC GTG TCA CTT CCC GGG GAA GGC TAC AGT ACA 6422
Arg Ala Glu Glu Asp Gly Val Ser Leu Pro Gly Glu Gly Tyr Ser Thr
2060 2065 2070

20 TTC ATG GCA AAC AGT GGA CTC CCG GAC AAA TCA GAA ACT GCC TCT GCT 6470
Phe Met Ala Asn Ser Gly Leu Pro Asp Lys Ser Glu Thr Ala Ser Ala
2075 2080 2085

25 ACG TCT TTC CCG CCA TCC TAT GAC AGT GTC ACC AGG GGC CTG AGT GAC 6518
Thr Ser Phe Pro Pro Ser Tyr Asp Ser Val Thr Arg Gly Leu Ser Asp
2090 2095 2100 2105

30 CGG GCC AAC ATT AAC CCA TCT AGC TCA ATG CAA AAT GAA GAT GAG GTC 6566
Arg Ala Asn Ile Asn Pro Ser Ser Ser Met Gln Asn Glu Asp Glu Val
2110 2115 2120

35 GCT GCT AAG GAA GGA AAC AGC CCT GGA CCT CAG TGAAGGCACT CAGGCATGCA 6619
Ala Ala Lys Glu Gly Asn Ser Pro Gly Pro Gln
2125 2130

CAGGGCAGGT TCCAATGTCT TTCTCTGCTG TACTAACTCC TTCCCTCTGG AGGTGGCACC 6679

40 AACCTCCAGC CTCCACCAAT GCATGTCACT GGTCATGGTG TCAGAACTGA ATGGGGACAT 6739

CCTTGAGAAA GCCCCCACCC CAATAGGAAT CAAAAGCCAA GGATACTCCT CCATTCTGAC 6799

45 GTCCCTTCCG AGTTCCGAGA AGATGTCACT GCTCCCTTCT GTTTGTGACC AGAGACGTGA 6859

TTCACCAACT TCTCGGAGCC AGAGACACAT AGCAAAGACT TTTCTGCTGG TGTCGGGCAG 6919

TCTTAGAGAA GTCACGTAGG GGTTGGTACT GAGAATTAGG GTTTCATGA CTGCATGCTC 6979

50 ACAGCTGCCG GACAATACCT GTGAGTCGGC CATTAATAATT AATATTTTAA AAGTTAAAAA 7039

AAAAA AAA 7052

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2132 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met Glu Leu Pro Phe Ala Ser Val Gly Thr Thr Asn Phe Arg Arg Phe
1 5 10 15

Thr Pro Glu Ser Leu Ala Glu Ile Glu Lys Gln Ile Ala Ala His Arg
 20 25 30
 5 Ala Ala Lys Lys Ala Arg Thr Lys His Arg Gly Gln Glu Asp Lys Gly
 35 40 45
 Glu Lys Pro Arg Pro Gln Leu Asp Leu Lys Asp Cys Asn Gln Leu Pro
 50 55 60
 10 Lys Phe Tyr Gly Glu Leu Pro Ala Glu Leu Val Gly Glu Pro Leu Glu
 65 70 75 80
 Asp Leu Asp Pro Phe Tyr Ser Thr His Arg Thr Phe Met Val Leu Asn
 85 90 95
 15 Lys Ser Arg Thr Ile Ser Arg Phe Ser Ala Thr Trp Ala Leu Trp Leu
 100 105 110
 Phe Ser Pro Phe Asn Leu Ile Arg Arg Thr Ala Ile Lys Val Ser Val
 115 120 125
 20 His Ser Trp Phe Ser Ile Phe Ile Thr Ile Thr Ile Leu Val Asn Cys
 130 135 140
 25 Val Cys Met Thr Arg Thr Asp Leu Pro Glu Lys Val Glu Tyr Val Phe
 145 150 155 160
 Thr Val Ile Tyr Thr Phe Glu Ala Leu Ile Lys Ile Leu Ala Arg Gly
 165 170 175
 30 Phe Cys Leu Asn Glu Phe Thr Tyr Leu Arg Asp Pro Trp Asn Trp Leu
 180 185 190
 35 Asp Phe Ser Val Ile Thr Leu Ala Tyr Val Gly Ala Ala Ile Asp Leu
 195 200 205
 Arg Gly Ile Ser Gly Leu Arg Thr Phe Arg Val Leu Arg Ala Leu Lys
 210 215 220
 40 Thr Val Ser Val Ile Pro Gly Leu Lys Val Ile Val Gly Ala Leu Ile
 225 230 235 240
 His Ser Val Arg Lys Leu Ala Asp Val Thr Ile Leu Thr Val Phe Cys
 245 250 255
 45 Leu Ser Val Phe Ala Leu Val Gly Leu Gln Leu Phe Lys Gly Asn Leu
 260 265 270
 Lys Asn Lys Cys Ile Arg Asn Gly Thr Asp Pro His Lys Ala Asp Asn
 275 280 285
 50 Leu Ser Ser Glu Met Ala Glu Tyr Ile Phe Ile Lys Pro Gly Thr Thr
 290 295 300
 55 Asp Pro Leu Leu Cys Gly Asn Gly Ser Asp Ala Gly His Cys Pro Gly
 305 310 315 320
 Gly Tyr Val Cys Leu Lys Thr Pro Asp Asn Pro Asp Phe Asn Tyr Thr
 325 330 335
 60 Ser Phe Asp Ser Phe Ala Trp Ala Phe Leu Ser Leu Phe Arg Leu Met
 340 345 350

Thr Gln Asp Ser Trp Glu Arg Leu Tyr Gln Gln Thr Leu Arg Ala Ser
355 360 365

5 Gly Lys Met Tyr Met Val Phe Phe Val Leu Val Ile Phe Leu Gly Ser
370 375 380

Phe Tyr Leu Val Asn Leu Ile Leu Ala Val Val Thr Met Ala Tyr Glu
385 390 395 400

10 Glu Gln Ser Gln Ala Thr Ile Ala Glu Ile Glu Ala Lys Glu Lys Lys
405 410 415

Phe Gln Glu Ala Leu Glu Val Leu Gln Lys Glu Gln Glu Val Leu Ala
420 425 430

15 Ala Leu Gly Ile Asp Thr Thr Ser Leu Gln Ser His Ser Gly Ser Pro
435 440 445

20 Leu Ala Ser Lys Asn Ala Asn Glu Arg Arg Pro Arg Val Lys Ser Arg
450 455 460

Val Ser Glu Gly Ser Thr Asp Asp Asn Arg Ser Pro Gln Ser Asp Pro
465 470 475 480

25 Tyr Asn Gln Arg Arg Met Ser Phe Leu Gly Leu Ser Ser Gly Arg Arg
485 490 495

Arg Ala Ser His Gly Ser Val Phe His Phe Arg Ala Pro Ser Gln Asp
500 505 510

30 Ile Ser Phe Pro Asp Gly Ile Thr Pro Asp Asp Gly Val Phe His Gly
515 520 525

35 Asp Gln Glu Ser Arg Arg Gly Ser Ile Leu Leu Gly Arg Gly Ala Gly
530 535 540

Gln Thr Gly Pro Leu Pro Arg Ser Pro Leu Pro Gln Ser Pro Asn Pro
545 550 555 560

40 Gly Arg Arg His Gly Glu Glu Gly Gln Leu Gly Val Pro Thr Gly Glu
565 570 575

Leu Thr Ala Gly Ala Pro Glu Gly Pro Ala Leu Asp Thr Thr Gly Gln
580 585 590

45 Lys Ser Phe Leu Ser Ala Gly Tyr Leu Asn Glu Pro Phe Arg Ala Gln
595 600 605

Arg Ala Met Ser Val Val Ser Ile Met Thr Ser Val Ile Glu Glu Leu
610 615 620

50 Glu Glu Ser Lys Leu Lys Cys Pro Pro Cys Leu Ile Ser Phe Ala Gln
625 630 635 640

55 Lys Tyr Leu Ile Trp Glu Cys Cys Pro Lys Trp Arg Lys Phe Lys Met
645 650 655

Ala Leu Phe Glu Leu Val Thr Asp Pro Phe Ala Glu Leu Thr Ile Thr
660 665 670

60 Leu Cys Ile Val Val Asn Thr Val Phe Met Ala Met Glu His Tyr Pro
675 680 685

Met Thr Asp Ala Phe Asp Ala Met Leu Gln Ala Gly Asn Ile Val Phe
 690 695 700
 5 Thr Val Phe Phe Thr Met Glu Met Ala Phe Lys Ile Ile Ala Phe Asp
 705 710 715 720
 Pro Tyr Tyr Tyr Phe Gln Lys Lys Trp Asn Ile Phe Asp Cys Val Ile
 725 730 735
 10 Val Thr Val Ser Leu Leu Glu Leu Ser Ala Ser Lys Lys Gly Ser Leu
 740 745 750
 Ser Val Leu Arg Ser Leu Arg Leu Ala Leu Asp Thr Thr Gly Gln Lys
 755 760 765
 15 Ser Phe Leu Ser Ala Gly Tyr Leu Asn Glu Pro Phe Arg Ala Gln Arg
 770 775 780
 20 Ala Met Ser Val Val Ser Ile Met Thr Ser Val Ile Glu Glu Leu Glu
 785 790 795 800
 Glu Ser Lys Leu Lys Cys Pro Pro Cys Leu Ile Ser Phe Ala Gln Lys
 805 810 815
 25 Tyr Leu Ile Trp Glu Cys Cys Pro Lys Trp Arg Lys Phe Lys Met Ala
 820 825 830
 Leu Phe Glu Leu Val Thr Asp Pro Phe Ala Glu Leu Thr Ile Thr Leu
 835 840 845
 30 Cys Ile Val Val Asn Thr Val Phe Met Ala Met Glu His Tyr Pro Met
 850 855 860
 35 Thr Asp Ala Phe Asp Ala Met Leu Gln Ala Gly Asn Ile Val Phe Thr
 865 870 875 880
 Val Phe Phe Thr Met Glu Met Ala Phe Lys Ile Ile Ala Phe Asp Pro
 885 890 895
 40 Tyr Tyr Tyr Phe Gln Lys Lys Trp Asn Ile Phe Asp Cys Val Ile Val
 900 905 910
 Thr Val Ser Leu Leu Glu Leu Ser Ala Ser Lys Lys Gly Ser Leu Ser
 915 920 925
 45 Val Leu Arg Ser Leu Arg Leu Leu Arg Val Phe Lys Leu Ala Lys Ser
 930 935 940
 50 Trp Pro Thr Leu Asn Thr Leu Ile Lys Ile Ile Gly Asn Ser Val Gly
 945 950 955 960
 Ala Leu Gly Asn Leu Thr Phe Ile Leu Ala Ile Ile Val Phe Ile Phe
 965 970 975
 55 Ala Leu Val Gly Lys Gln Leu Leu Ser Glu Asp Tyr Gly Cys Arg Lys
 980 985 990
 60 Asp Gly Val Ser Val Trp Asn Gly Glu Lys Leu Arg Trp His Met Cys
 995 1000 1005
 Asp Phe Phe His Ser Phe Leu Val Val Phe Arg Ile Leu Cys Gly Glu
 1010 1015 1020

Trp Ile Glu Asn Met Trp Val Cys Met Glu Val Ser Gln Lys Ser Ile
 1025 1030 1035 1040
 5 Cys Leu Ile Leu Phe Leu Thr Val Met Val Leu Gly Asn Leu Val Val
 1045 1050 1055
 Leu Asn Leu Phe Ile Ala Leu Leu Leu Asn Ser Phe Ser Ala Asp Asn
 1060 1065 1070
 10 Leu Thr Ala Pro Glu Asp Asp Gly Glu Val Asn Asn Leu Gln Leu Ala
 1075 1080 1085
 Leu Ala Arg Ile Gln Val Leu Gly His Arg Ala Ser Arg Ala Ile Ala
 1090 1095 1100
 15 Ser Tyr Ile Ser Ser His Cys Arg Phe Arg Trp Pro Lys Val Glu Thr
 1105 1110 1115 1120
 Gln Leu Gly Met Lys Pro Pro Leu Thr Ser Ser Glu Ala Lys Asn His
 1125 1130 1135
 20 Ile Ala Thr Asp Ala Val Ser Ala Ala Val Gly Asn Leu Thr Lys Pro
 1140 1145 1150
 25 Ala Leu Ser Ser Pro Lys Glu Asn His Gly Asp Phe Ile Thr Asp Pro
 1155 1160 1165
 Asn Val Trp Val Ser Val Pro Ile Ala Glu Gly Glu Ser Asp Leu Asp
 1170 1175 1180
 30 Glu Leu Glu Glu Asp Met Glu Gln Ala Ser Gln Ser Ser Trp Gln Glu
 1185 1190 1195 1200
 35 Glu Asp Pro Lys Gly Gln Gln Glu Gln Leu Pro Gln Val Gln Lys Cys
 1205 1210 1215
 Glu Asn His Gln Ala Ala Arg Ser Pro Ala Ser Met Met Ser Ser Glu
 1220 1225 1230
 40 Asp Leu Ala Pro Tyr Leu Gly Glu Ser Trp Lys Arg Lys Asp Ser Pro
 1235 1240 1245
 Gln Val Pro Ala Glu Gly Val Asp Asp Thr Ser Ser Ser Glu Gly Ser
 1250 1255 1260
 45 Thr Val Asp Cys Pro Asp Pro Glu Glu Ile Leu Arg Lys Ile Pro Glu
 1265 1270 1275 1280
 Leu Ala Asp Asp Leu Asp Glu Pro Asp Asp Cys Phe Thr Glu Gly Cys
 1285 1290 1295
 50 Thr Arg Arg Cys Pro Cys Cys Asn Val Asn Thr Ser Lys Ser Pro Trp
 1300 1305 1310
 55 Ala Thr Gly Trp Gln Val Arg Lys Thr Cys Tyr Arg Ile Val Glu His
 1315 1320 1325
 Ser Trp Phe Glu Ser Phe Ile Ile Phe Met Ile Leu Leu Ser Ser Gly
 1330 1335 1340
 60 Ala Leu Ala Phe Glu Asp Asn Tyr Leu Glu Glu Lys Pro Arg Val Lys
 1345 1350 1355 1360
 Ser Val Leu Glu Tyr Thr Asp Arg Val Phe Thr Phe Ile Phe Val Phe
 1365 1370 1375

Glu Met Leu Leu Lys Trp Val Ala Tyr Gly Phe Lys Lys Tyr Phe Thr
 1380 1385 1390
 5 Asn Ala Trp Cys Trp Leu Asp Phe Leu Ile Val Asn Ile Ser Leu Thr
 1395 1400 1405
 Ser Leu Ile Ala Lys Ile Leu Glu Tyr Ser Asp Val Ala Ser Ile Lys
 1410 1415 1420
 10 Ala Leu Arg Thr Leu Arg Ala Leu Arg Pro Leu Arg Ala Leu Ser Arg
 1425 1430 1435 1440
 Phe Glu Gly Met Arg Val Val Val Asp Ala Leu Val Gly Ala Ile Pro
 1445 1450 1455
 Ser Ile Met Asn Val Leu Leu Val Cys Leu Ile Phe Trp Leu Ile Phe
 1460 1465 1470
 20 Ser Ile Met Gly Val Asn Leu Phe Ala Gly Lys Phe Ser Lys Cys Val
 1475 1480 1485
 Asp Thr Arg Asn Asn Pro Phe Ser Asn Val Asn Ser Thr Met Val Asn
 1490 1495 1500
 25 Asn Lys Ser Glu Cys His Asn Gln Asn Ser Thr Gly His Phe Phe Trp
 1505 1510 1515 1520
 Val Asn Val Lys Val Asn Phe Asp Asn Val Ala Met Gly Tyr Leu Ala
 1525 1530 1535
 Leu Leu Gln Val Ala Thr Phe Lys Gly Trp Met Asp Ile Met Tyr Ala
 1540 1545 1550
 35 Ala Val Asp Ser Gly Glu Ile Asn Ser Gln Pro Asn Trp Glu Asn Asn
 1555 1560 1565
 Leu Tyr Met Tyr Leu Tyr Phe Val Val Phe Ile Ile Phe Gly Gly Phe
 1570 1575 1580
 40 Phe Thr Leu Asn Leu Phe Val Gly Val Ile Ile Asp Asn Phe Asn Gln
 1585 1590 1595 1600
 Gln Lys Lys Lys Leu Gly Gly Gln Asp Ile Phe Met Thr Glu Glu Gln
 1605 1610 1615
 45 Lys Lys Tyr Tyr Asn Ala Met Lys Lys Leu Gly Ser Lys Lys Pro Gln
 1620 1625 1630
 50 Lys Pro Ile Pro Arg Pro Leu Asn Lys Tyr Gln Gly Phe Val Phe Asp
 1635 1640 1645
 Ile Val Thr Arg Gln Ala Phe Asp Ile Ile Ile Met Val Leu Ile Cys
 1650 1655 1660
 55 Leu Asn Met Ile Thr Met Met Val Glu Thr Asp Glu Gln Gly Glu Glu
 1665 1670 1675 1680
 Lys Thr Lys Val Leu Gly Arg Ile Asn Gln Phe Phe Val Ala Val Phe
 1685 1690 1695
 60 Thr Gly Glu Cys Val Met Lys Met Phe Ala Leu Arg Gln Tyr Tyr Phe
 1700 1705 1710

Thr Asn Gly Trp Asn Val Phe Asp Phe Ile Val Val Ile Leu Ser Ile
 1715 1720 1725
 5 Gly Ser Leu Leu Phe Ser Ala Ile Leu Lys Ser Leu Glu Asn Tyr Phe
 1730 1735 1740
 Ser Pro Thr Leu Phe Arg Val Ile Arg Leu Ala Arg Ile Gly Arg Ile
 1745 1750 1755 1760
 10 Leu Arg Leu Ile Arg Ala Ala Lys Gly Ile Arg Thr Leu Leu Phe Ala
 1765 1770 1775
 Leu Met Met Ser Leu Pro Ala Leu Phe Asn Ile Gly Leu Leu Leu Phe
 1780 1785 1790
 15 Leu Val Met Phe Ile Tyr Ser Ile Phe Gly Met Ala Ser Phe Ala Asn
 1795 1800 1805
 20 Val Val Asp Glu Ala Gly Ile Asp Asp Met Phe Asn Phe Lys Thr Phe
 1810 1815 1820
 Gly Asn Ser Met Leu Cys Leu Phe Gln Ile Thr Thr Ser Ala Gly Trp
 1825 1830 1835 1840
 25 Asp Gly Leu Leu Ser Pro Ile Leu Asn Thr Gly Pro Pro Tyr Cys Asp
 1845 1850 1855
 Pro Asn Leu Pro Asn Ser Asn Gly Ser Arg Gly Asn Cys Gly Ser Pro
 1860 1865 1870
 30 Ala Val Gly Ile Ile Phe Phe Thr Thr Tyr Ile Ile Ile Ser Phe Leu
 1875 1880 1885
 35 Ile Val Val Asn Met Tyr Ile Ala Val Ile Leu Glu Asn Phe Asn Val
 1890 1895 1900
 Ala Thr Glu Glu Ser Thr Glu Pro Leu Ser Glu Asp Asp Phe Asp Met
 1905 1910 1915 1920
 40 Phe Tyr Glu Thr Trp Glu Lys Phe Asp Pro Glu Ala Thr Gln Phe Ile
 1925 1930 1935
 45 Ala Phe Ser Ala Leu Ser Asp Phe Ala Asp Thr Leu Ser Gly Pro Leu
 1940 1945 1950
 Arg Ile Pro Lys Pro Asn Gln Asn Ile Leu Ile Gln Met Asp Leu Pro
 1955 1960 1965
 50 Leu Val Pro Gly Asp Lys Ile His Cys Leu Asp Ile Leu Phe Ala Phe
 1970 1975 1980
 Thr Lys Asn Val Leu Gly Glu Ser Gly Glu Leu Asp Ser Leu Lys Thr
 1985 1990 1995 2000
 55 Asn Met Glu Glu Lys Phe Met Ala Thr Asn Leu Ser Lys Ala Ser Tyr
 2005 2010 2015
 60 Glu Pro Ile Ala Thr Thr Leu Arg Trp Lys Gln Glu Asp Leu Ser Ala
 2020 2025 2030
 Thr Val Ile Gln Lys Ala Tyr Arg Ser Tyr Met Leu His Arg Ser Leu
 2035 2040 2045

Thr Leu Ser Asn Thr Leu His Val Pro Arg Ala Glu Glu Asp Gly Val
 2050 2055 2060
 5 Ser Leu Pro Gly Glu Gly Tyr Ser Thr Phe Met Ala Asn Ser Gly Leu
 2065 2070 2075 2080
 Pro Asp Lys Ser Glu Thr Ala Ser Ala Thr Ser Phe Pro Pro Ser Tyr
 2085 2090 2095
 10 Asp Ser Val Thr Arg Gly Leu Ser Asp Arg Ala Asn Ile Asn Pro Ser
 2100 2105 2110
 Ser Ser Met Gln Asn Glu Asp Glu Val Ala Ala Lys Glu Gly Asn Ser
 2115 2120 2125
 15 Pro Gly Pro Gln
 2130
 20 (2) INFORMATION FOR SEQ ID NO:7:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 6527 base pairs
 (B) TYPE: nucleic acid
 25 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: cDNA
 30 (ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 204..6077
 35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:
 TAGCTTGCTT CTGCTAATGC TACCCAGGC CTTTAGACAG AGAACAGATG GCAGATGGAG 60
 40 TTTCTTATTG CCATGCGCAA ACGCTGAGCC CACCTCATGA TCCCGGACCC CATGGTTTTC 120
 AGTAGACAAC CTGGGCTAAG AAGAGATCTC CGACCTTATA GAGCAGCAAA GAGTGTAAT 180
 TCTTCCCCAA GAAGAATGAG AAG ATG GAG CTC CCC TTT GCG TCC GTG GGA 230
 45 Met Glu Leu Pro Phe Ala Ser Val Gly
 1 5
 ACT ACC AAT TTC AGA CGG TTC ACT CCA GAG TCA CTG GCA GAG ATC GAG 278
 50 Thr Thr Asn Phe Arg Arg Phe Thr Pro Glu Ser Leu Ala Glu Ile Glu
 10 15 20 25
 AAG CAG ATT GCT GCT CAC CGG GCA GCC AAG AAG GCC AGA ACC AAG CAC 326
 Lys Gln Ile Ala Ala His Arg Ala Ala Lys Lys Ala Arg Thr Lys His
 30 35 40
 55 AGA GGA CAG GAG GAC AAG GGC GAG AAG CCC AGG CCT CAG CTG GAC TTG 374
 Arg Gly Gln Glu Asp Lys Gly Glu Lys Pro Arg Pro Gln Leu Asp Leu
 45 50 55
 60 AAA GAC TGT AAC CAG CTG CCC AAG TTC TAT GGT GAG CTC CCA GCA GAA 422
 Lys Asp Cys Asn Gln Leu Pro Lys Phe Tyr Gly Glu Leu Pro Ala Glu
 60 65 70

	CTG	GTC	GGG	GAG	CCC	CTG	GAG	GAC	CTA	GAC	CCT	TTC	TAC	AGC	ACA	CAC	470
	Leu	Val	Gly	Glu	Pro	Leu	Glu	Asp	Leu	Asp	Pro	Phe	Tyr	Ser	Thr	His	
		75					80					85					
5	CGG	ACA	TTC	ATG	GTG	TTG	AAT	AAA	AGC	AGG	ACC	ATT	TCC	AGA	TTC	AGT	518
	Arg	Thr	Phe	Met	Val	Leu	Asn	Lys	Ser	Arg	Thr	Ile	Ser	Arg	Phe	Ser	
	90					95					100					105	
10	GCC	ACT	TGG	GCC	CTG	TGG	CTC	TTC	AGT	CCC	TTC	AAC	CTG	ATC	AGA	AGA	566
	Ala	Thr	Trp	Ala	Leu	Trp	Leu	Phe	Ser	Pro	Phe	Asn	Leu	Ile	Arg	Arg	
					110					115					120		
15	ACA	GCC	ATC	AAA	GTG	TCT	GTC	CAT	TCC	TGG	TTC	TCC	ATA	TTC	ATC	ACC	614
	Thr	Ala	Ile	Lys	Val	Ser	Val	His	Ser	Trp	Phe	Ser	Ile	Phe	Ile	Thr	
				125					130					135			
	ATC	ACT	ATT	TTG	GTC	AAC	TGC	GTG	TGC	ATG	ACC	CGA	ACT	GAT	CTT	CCA	662
	Ile	Thr	Ile	Leu	Val	Asn	Cys	Val	Cys	Met	Thr	Arg	Thr	Asp	Leu	Pro	
			140				145						150				
20	GAG	AAA	GTC	GAG	TAC	GTC	TTC	ACT	GTC	ATT	TAC	ACC	TTC	GAG	GCT	CTG	710
	Glu	Lys	Val	Glu	Tyr	Val	Phe	Thr	Val	Ile	Tyr	Thr	Phe	Glu	Ala	Leu	
		155					160					165					
25	ATT	AAG	ATA	CTG	GCA	AGA	GGG	TTT	TGT	CTA	AAT	GAG	TTC	ACT	TAT	CTT	758
	Ile	Lys	Ile	Leu	Ala	Arg	Gly	Phe	Cys	Leu	Asn	Glu	Phe	Thr	Tyr	Leu	
	170					175					180					185	
30	CGA	GAT	CCG	TGG	AAC	TGG	CTG	GAC	TTC	AGT	GTC	ATT	ACC	TTG	GCG	TAT	806
	Arg	Asp	Pro	Trp	Asn	Trp	Leu	Asp	Phe	Ser	Val	Ile	Thr	Leu	Ala	Tyr	
					190				195						200		
35	GTG	GGT	GCA	GCG	ATA	GAC	CTC	CGA	GGA	ATC	TCA	GGC	CTG	CGG	ACA	TTC	854
	Val	Gly	Ala	Ala	Ile	Asp	Leu	Arg	Gly	Ile	Ser	Gly	Leu	Arg	Thr	Phe	
				205					210				215				
	CGA	GTT	CTC	AGA	GCC	CTG	AAA	ACT	GTT	TCT	GTG	ATC	CCA	GGA	CTG	AAG	902
	Arg	Val	Leu	Arg	Ala	Leu	Lys	Thr	Val	Ser	Val	Ile	Pro	Gly	Leu	Lys	
			220				225						230				
40	GTC	ATC	GTG	GGA	GCC	CTG	ATC	CAC	TCA	GTG	AGG	AAG	CTG	GCC	GAC	GTG	950
	Val	Ile	Val	Gly	Ala	Leu	Ile	His	Ser	Val	Arg	Lys	Leu	Ala	Asp	Val	
		235					240					245					
45	ACT	ATC	CTC	ACA	GTC	TTC	TGC	CTG	AGC	GTC	TTC	GCC	TTC	GTG	GGC	CTG	998
	Thr	Ile	Leu	Thr	Val	Phe	Cys	Leu	Ser	Val	Phe	Ala	Leu	Val	Gly	Leu	
	250					255					260				265		
50	CAG	CTC	TTT	AAG	GGG	AAC	CTT	AAG	AAC	AAA	TGC	ATC	AGG	AAC	GGA	ACA	1046
	Gln	Leu	Phe	Lys	Gly	Asn	Leu	Lys	Asn	Lys	Cys	Ile	Arg	Asn	Gly	Thr	
					270					275					280		
55	GAT	CCC	CAC	AAG	GCT	GAC	AAC	CTC	TCA	TCT	GAA	ATG	GCA	GAA	TAC	ATC	1094
	Asp	Pro	His	Lys	Ala	Asp	Asn	Leu	Ser	Ser	Glu	Met	Ala	Glu	Tyr	Ile	
				285					290					295			
	TTC	ATC	AAG	CCT	GGT	ACT	ACG	GAT	CCC	TTA	CTG	TGC	GGC	AAT	GGG	TCT	1142
	Phe	Ile	Lys	Pro	Gly	Thr	Thr	Asp	Pro	Leu	Leu	Cys	Gly	Asn	Gly	Ser	
			300					305					310				
60	GAT	GCT	GGT	CAC	TGC	CCT	GGA	GGC	TAT	GTC	TGC	CTG	AAA	ACT	CCT	GAC	1190
	Asp	Ala	Gly	His	Cys	Pro	Gly	Gly	Tyr	Val	Cys	Leu	Lys	Thr	Pro	Asp	
		315					320					325					

	AAC	CCG	GAT	TTT	AAC	TAC	ACC	AGC	TTT	GAT	TCC	TTT	GCG	TGG	GCA	TTC	1238
	Asn	Pro	Asp	Phe	Asn	Tyr	Thr	Ser	Phe	Asp	Ser	Phe	Ala	Trp	Ala	Phe	
	330					335					340					345	
5	CTC	TCA	CTG	TTC	CGC	CTC	ATG	ACG	CAG	GAC	TCC	TGG	GAG	CGC	CTG	TAC	1286
	Leu	Ser	Leu	Phe	Arg	Leu	Met	Thr	Gln	Asp	Ser	Trp	Glu	Arg	Leu	Tyr	
					350					355					360		
10	CAG	CAG	ACA	CTC	CGG	GCT	TCT	GGG	AAA	ATG	TAC	ATG	GTC	TTT	TTC	GTG	1334
	Gln	Gln	Thr	Leu	Arg	Ala	Ser	Gly	Lys	Met	Tyr	Met	Val	Phe	Phe	Val	
				365					370					375			
15	CTG	GTT	ATT	TTC	CTT	GGA	TCG	TTC	TAC	CTG	GTC	AAT	TTG	ATC	TTG	GCC	1382
	Leu	Val	Ile	Phe	Leu	Gly	Ser	Phe	Tyr	Leu	Val	Asn	Leu	Ile	Leu	Ala	
			380					385					390				
20	GTG	GTC	ACC	ATG	GCG	TAT	GAA	GAG	CAG	AGC	CAG	GCA	ACA	ATT	GCA	GAA	1430
	Val	Val	Thr	Met	Ala	Tyr	Glu	Glu	Gln	Ser	Gln	Ala	Thr	Ile	Ala	Glu	
		395				400						405					
25	ATC	GAA	GCC	AAG	GAA	AAA	AAG	TTC	CAG	GAA	GCC	CTT	GAG	GTG	CTG	CAG	1478
	Ile	Glu	Ala	Lys	Glu	Lys	Lys	Phe	Gln	Glu	Ala	Leu	Glu	Val	Leu	Gln	
	410					415					420					425	
30	AAG	GAA	CAG	GAG	GTG	CTG	GCA	GCC	CTG	GGG	ATT	GAC	ACG	ACC	TCG	CTC	1526
	Lys	Glu	Gln	Glu	Val	Leu	Ala	Ala	Leu	Gly	Ile	Asp	Thr	Thr	Ser	Leu	
					430					435					440		
35	CAG	TCC	CAC	AGT	GGA	TCA	CCC	TTA	GCC	TCC	AAA	AAC	GCC	AAT	GAG	AGA	1574
	Gln	Ser	His	Ser	Gly	Ser	Pro	Leu	Ala	Ser	Lys	Asn	Ala	Asn	Glu	Arg	
				445				450						455			
40	AGA	CCC	AGG	GTG	AAA	TCA	AGG	GTG	TCA	GAG	GGC	TCC	ACG	GAT	GAC	AAC	1622
	Arg	Pro	Arg	Val	Lys	Ser	Arg	Val	Ser	Glu	Gly	Ser	Thr	Asp	Asp	Asn	
			460					465					470				
45	AGG	TCA	CCC	CAA	TCT	GAC	CCT	TAC	AAC	CAG	CGC	AGG	ATG	TCT	TTC	CTA	1670
	Arg	Ser	Pro	Gln	Ser	Asp	Pro	Tyr	Asn	Gln	Arg	Arg	Met	Ser	Phe	Leu	
		475					480					485					
50	GGC	CTG	TCT	TCA	GGA	AGA	CGC	AGG	GCT	ACC	CAC	GGC	AGT	GTG	TTC	CAC	1718
	Gly	Leu	Ser	Ser	Gly	Arg	Arg	Arg	Ala	Ser	His	Gly	Ser	Val	Phe	His	
	490					495					500					505	
55	TTC	CGA	GCG	CCC	AGC	CAA	GAC	ATC	TCA	TTT	CCT	GAC	GGG	ATC	ACC	CCT	1766
	Phe	Arg	Ala	Pro	Ser	Gln	Asp	Ile	Ser	Phe	Pro	Asp	Gly	Ile	Thr	Pro	
					510				515						520		
60	GAT	GAT	GGG	GTC	TTT	CAC	GGA	GAC	CAG	GAA	AGC	CGT	CGA	GGT	TCC	ATA	1814
	Asp	Asp	Gly	Val	Phe	His	Gly	Asp	Gln	Glu	Ser	Arg	Arg	Gly	Ser	Ile	
				525					530					535			
65	TTG	CTG	GGC	AGG	GGT	GCT	GGG	CAG	ACA	GGT	CCA	CTC	CCC	AGG	AGC	CCA	1862
	Leu	Leu	Gly	Arg	Gly	Ala	Gly	Gln	Thr	Gly	Pro	Leu	Pro	Arg	Ser	Pro	
			540					545					550				
70	CTG	CCT	CAG	TCC	CCC	AAC	CCT	GGC	CGT	AGA	CAT	GGA	GAA	GAG	GGA	CAG	1910
	Leu	Pro	Gln	Ser	Pro	Asn	Pro	Gly	Arg	Arg	His	Gly	Glu	Glu	Gly	Gln	
		555					560					565					
75	CTC	GGA	GTG	CCC	ACT	GGT	GAG	CTT	ACC	GCT	GGA	GCG	CCT	GAA	GGC	CCG	1958
	Leu	Gly	Val	Pro	Thr	Gly	Glu	Leu	Thr	Ala	Gly	Ala	Pro	Glu	Gly	Pro	
						575					580					585	

	GCA	CTC	GAC	ACT	ACA	GGG	CAG	AAG	AGC	TTC	CTG	TCT	GCG	GGC	TAC	TTG	2006
	Ala	Leu	Asp	Thr	Thr	Gly	Gln	Lys	Ser	Phe	Leu	Ser	Ala	Gly	Tyr	Leu	
					590					595					600		
5	AAC	GAA	CCT	TTC	CGA	GCA	CAG	AGG	GCC	ATG	AGC	GTT	GTC	AGT	ATC	ATG	2054
	Asn	Glu	Pro	Phe	Arg	Ala	Gln	Arg	Ala	Met	Ser	Val	Val	Ser	Ile	Met	
				605					610					615			
10	ACT	TCT	GTC	ATT	GAG	GAG	CTT	GAA	GAG	TCT	AAG	CTG	AAG	TGC	CCA	CCC	2102
	Thr	Ser	Val	Ile	Glu	Glu	Leu	Glu	Glu	Ser	Lys	Leu	Lys	Cys	Pro	Pro	
			620					625					630				
15	TGC	TTG	ATC	AGC	TTC	GCT	CAG	AAG	TAT	CTG	ATC	TGG	GAG	TGC	TGC	CCC	2150
	Cys	Leu	Ile	Ser	Phe	Ala	Gln	Lys	Tyr	Leu	Ile	Trp	Glu	Cys	Cys	Pro	
		635					640					645					
20	AAG	TGG	AGG	AAG	TTC	AAG	ATG	GCG	CTG	TTC	GAG	CTG	GTG	ACT	GAC	CCC	2198
	Lys	Trp	Arg	Lys	Phe	Lys	Met	Ala	Leu	Phe	Glu	Leu	Val	Thr	Asp	Pro	
		650				655					660					665	
25	TTC	GCA	GAG	CTT	ACC	ATC	ACC	CTC	TGC	ATC	GTG	GTG	AAC	ACC	GTC	TTC	2246
	Phe	Ala	Glu	Leu	Thr	Ile	Thr	Leu	Cys	Ile	Val	Val	Asn	Thr	Val	Phe	
				670					675						680		
30	ATG	GCC	ATG	GAG	CAC	TAC	CCC	ATG	ACC	GAT	GCC	TTC	GAT	GCC	ATG	CTT	2294
	Met	Ala	Met	Glu	His	Tyr	Pro	Met	Thr	Asp	Ala	Phe	Asp	Ala	Met	Leu	
				685				690						695			
35	CAA	GCC	GGC	AAC	ATT	GTC	TTC	ACC	GTG	TTT	TTC	ACA	ATG	GAG	ATG	GCC	2342
	Gln	Ala	Gly	Asn	Ile	Val	Phe	Thr	Val	Phe	Phe	Thr	Met	Glu	Met	Ala	
			700					705					710				
40	TTC	AAG	ATC	ATT	GCC	TTC	GAC	CCC	TAC	TAT	TAC	TTC	CAG	AAG	AAG	TGG	2390
	Phe	Lys	Ile	Ile	Ala	Phe	Asp	Pro	Tyr	Tyr	Tyr	Phe	Gln	Lys	Lys	Trp	
		715					720					725					
45	AAT	ATC	TTC	GAC	TGT	GTC	ATC	GTC	ACC	GTG	ACC	CTT	CTG	GAG	CTG	AGT	2438
	Asn	Ile	Phe	Asp	Cys	Val	Ile	Val	Thr	Val	Ser	Leu	Leu	Glu	Leu	Ser	
		730				735				740						745	
50	GCA	TCC	AAG	AAG	GGC	AGC	CTG	TCT	GTG	CTC	CGT	TCC	TTA	CGC	TTG	CTG	2486
	Ala	Ser	Lys	Lys	Gly	Ser	Leu	Ser	Val	Leu	Arg	Ser	Leu	Arg	Leu	Leu	
				750						755					760		
55	CGG	GTC	TTC	AAG	CTG	GCC	AAG	TCC	TGG	CCC	ACC	CTG	AAC	ACC	CTC	ATC	2534
	Arg	Val	Phe	Lys	Leu	Ala	Lys	Ser	Trp	Pro	Thr	Leu	Asn	Thr	Leu	Ile	
				765				770						775			
60	AAG	ATC	ATC	GGG	AAC	TCA	GTG	GGG	GCC	CTG	GGC	AAC	CTG	ACC	TTT	ATC	2582
	Lys	Ile	Ile	Gly	Asn	Ser	Val	Gly	Ala	Leu	Gly	Asn	Leu	Thr	Phe	Ile	
			780					785					790				
65	CTG	GCC	ATC	ATC	GTC	TTC	ATC	TTC	GCC	CTG	GTC	GGA	AAG	CAG	CTT	CTC	2630
	Leu	Ala	Ile	Ile	Val	Phe	Ile	Phe	Ala	Leu	Val	Gly	Lys	Gln	Leu	Leu	
		795					800					805					
70	TCA	GAG	GAC	TAC	GGG	TGC	CGC	AAG	GAC	GGC	GTC	TCC	GTG	TGG	AAC	GGC	2678
	Ser	Glu	Asp	Tyr	Gly	Cys	Arg	Lys	Asp	Gly	Val	Ser	Val	Trp	Asn	Gly	
		810				815					820					825	
75	GAG	AAG	CTC	CGC	TGG	CAC	ATG	TGT	GAC	TTC	TTC	CAT	TCC	TTC	CTG	GTC	2726
	Glu	Lys	Leu	Arg	Trp	His	Met	Cys	Asp	Phe	Phe	His	Ser	Phe	Leu	Val	
				830						835					840		

GTC TTC CGA ATC CTC TGC GGG GAG TGG ATC GAG AAC ATG TGG GTC TGC 2774
 Val Phe Arg Ile Leu Cys Gly Glu Trp Ile Glu Asn Met Trp Val Cys
 845 850 855

5 ATG GAG GTC AGC CAG AAA TCC ATC TGC CTC ATC CTC TTC TTG ACT GTG 2822
 Met Glu Val Ser Gln Lys Ser Ile Cys Leu Ile Leu Phe Leu Thr Val
 860 865 870

10 ATG GTG CTG GGC AAC CTA GTG GTG CTC AAC CTT TTC ATC GCT TTA CTG 2870
 Met Val Leu Gly Asn Leu Val Val Leu Asn Leu Phe Ile Ala Leu Leu
 875 880 885

15 CTG AAC TCC TTC AGC CCG GAC AAC CTC ACG GCT CCA GAG GAT GAC GGG 2918
 Leu Asn Ser Phe Ser Ala Asp Asn Leu Thr Ala Pro Glu Asp Asp Gly
 890 895 900 905

20 GAG GTG AAC AAC TTG CAG TTA GCA CTG GCC AGG ATC CAG GTA CTT GGC 2966
 Glu Val Asn Asn Leu Gln Leu Ala Leu Ala Arg Ile Gln Val Leu Gly
 910 915 920

CAT CGG GCC AGC AGG GCC ATC GCC AGT TAC ATC AGC AGC CAC TGC CGA 3014
 His Arg Ala Ser Arg Ala Ile Ala Ser Tyr Ile Ser Ser His Cys Arg
 925 930 935

25 TTC CGC TGG CCC AAG GTG GAG ACC CAG CTG GGC ATG AAG CCC CCA CTC 3062
 Phe Arg Trp Pro Lys Val Glu Thr Gln Leu Gly Met Lys Pro Pro Leu
 940 945 950

30 ACC AGC TCA GAG GCC AAG AAC CAC ATT GCC ACT GAT GCT GTC AGT GCT 3110
 Thr Ser Ser Glu Ala Lys Asn His Ile Ala Thr Asp Ala Val Ser Ala
 955 960 965

35 GCA GTG GGG AAC CTG ACA AAG CCA GCT CTC AGT AGC CCC AAG GAG AAT 3158
 Ala Val Gly Asn Leu Thr Lys Pro Ala Leu Ser Ser Pro Lys Glu Asn
 970 975 980 985

40 CAC GGG GAC TTC ATC ACT GAT CCC AAC GTG TGG GTC TCT GTG CCC ATT 3206
 His Gly Asp Phe Ile Thr Asp Pro Asn Val Trp Val Ser Val Pro Ile
 990 995 1000

GCT GAG GGG GAA TCT GAC CTC GAC GAG CTC GAG GAA GAT ATG GAG CAG 3254
 Ala Glu Gly Glu Ser Asp Leu Asp Glu Leu Glu Glu Asp Met Glu Gln
 1005 1010 1015

45 GCT TCG CAG AGC TCC TGG CAG GAA GAG GAC CCC AAG GGA CAG CAG CAG 3302
 Ala Ser Gln Ser Ser Trp Gln Glu Glu Asp Pro Lys Gly Gln Gln Glu
 1020 1025 1030

50 CAG TTG CCA CAA GTC CAA AAG TGT GAA AAC CAC CAG GCA GCC AGA AGC 3350
 Gln Leu Pro Gln Val Gln Lys Cys Glu Asn His Gln Ala Ala Arg Ser
 1035 1040 1045

55 CCA GCC TCC ATG ATG TCC TCT GAG GAC CTG GCT CCA TAC CTG GGT GAG 3398
 Pro Ala Ser Met Met Ser Ser Glu Asp Leu Ala Pro Tyr Leu Gly Glu
 1050 1055 1060 1065

AGC TGG AAG AGG AAG GAT AGC CCT CAG GTC CCT GCC GAG GGA GTG GAT 3446
 Ser Trp Lys Arg Lys Asp Ser Pro Gln Val Pro Ala Glu Gly Val Asp
 1070 1075 1080

60 GAC ACG AGC TCC TCT GAG GGC AGC ACG GTG GAC TGC CCG GAC CCA GAG 3494
 Asp Thr Ser Ser Ser Glu Gly Ser Thr Val Asp Cys Pro Asp Pro Glu
 1085 1090 1095

	GAA ATC CTG AGG AAG ATC CCC GAG CTG GCA GAT GAC CTG GAC GAG CCC	3542
	Glu Ile Leu Arg Lys Ile Pro Glu Leu Ala Asp Asp Leu Asp Glu Pro	
	1100 1105 1110	
5	GAT GAC TGT TTC ACA GAA GGC TGC ACT CGC CGC TGT CCC TGC TGC AAC	3590
	Asp Asp Cys Phe Thr Glu Gly Cys Thr Arg Arg Cys Pro Cys Cys Asn	
	1115 1120 1125	
10	GTG AAT ACT AGC AAG TCT CCT TGG GCC ACA GGC TGG CAG GTG CGC AAG	3638
	Val Asn Thr Ser Lys Ser Pro Trp Ala Thr Gly Trp Gln Val Arg Lys	
	1130 1135 1140 1145	
15	ACC TGC TAC CGC ATC GTG GAG CAC AGC TGG TTT GAG AGT TTC ATC ATC	3686
	Thr Cys Tyr Arg Ile Val Glu His Ser Trp Phe Glu Ser Phe Ile Ile	
	1150 1155 1160	
20	TTC ATG ATC CTG CTC AGC AGT GGA GCG CTG GCC TTT GAG GAT AAC TAC	3734
	Phe Met Ile Leu Leu Ser Ser Gly Ala Leu Ala Phe Glu Asp Asn Tyr	
	1165 1170 1175	
25	CTG GAA GAG AAA CCC CGA GTG AAG TCC GTG CTG GAG TAC ACT GAC CGA	3782
	Leu Glu Glu Lys Pro Arg Val Lys Ser Val Leu Glu Tyr Thr Asp Arg	
	1180 1185 1190	
30	GTG TTC ACC TTC ATC TTC GTC TTT GAG ATG CTG CTC AAG TGG GTA GCC	3830
	Val Phe Thr Phe Ile Phe Val Phe Glu Met Leu Leu Lys Trp Val Ala	
	1195 1200 1205	
35	TAT GGC TTC AAA AAG TAT TTC ACC AAT GCC TGG TGC TGG CTG GAC TTC	3878
	Tyr Gly Phe Lys Lys Tyr Phe Thr Asn Ala Trp Cys Trp Leu Asp Phe	
	1210 1215 1220 1225	
40	CTC ATT GTG AAC ATC TCC CTG ACA AGC CTC ATA GCG AAG ATC CTT GAG	3926
	Leu Ile Val Asn Ile Ser Leu Thr Ser Leu Ile Ala Lys Ile Leu Glu	
	1230 1235 1240	
45	TAT TCC GAC GTG GCG TCC ATC AAA GCC CTT CGG ACT CTC CGT GCC CTC	3974
	Tyr Ser Asp Val Ala Ser Ile Lys Ala Leu Arg Thr Leu Arg Ala Leu	
	1245 1250 1255	
50	CGA CCG CTG CGG GCT CTG TCT CGA TTC GAA GGC ATG AGG GTA GTG GTG	4022
	Arg Pro Leu Arg Ala Leu Ser Arg Phe Glu Gly Met Arg Val Val Val	
	1260 1265 1270	
55	GAT GCC CTC GTG GGC GCC ATC CCC TCC ATC ATG AAC GTC CTC CTC GTC	4070
	Asp Ala Leu Val Gly Ala Ile Pro Ser Ile Met Asn Val Leu Leu Val	
	1275 1280 1285	
60	TGC CTC ATC TTC TGG CTC ATC TTC AGC ATC ATG GGC GTG AAC CTC TTC	4118
	Cys Leu Ile Phe Trp Leu Ile Phe Ser Ile Met Gly Val Asn Leu Phe	
	1290 1295 1300 1305	
65	GCC GGG AAA TTT TCG AAG TGC GTC GAC ACC AGA AAT AAC CCA TTT TCC	4166
	Ala Gly Lys Phe Ser Lys Cys Val Asp Thr Arg Asn Asn Pro Phe Ser	
	1310 1315 1320	
70	AAC GTG AAT TCG ACG ATG GTG AAT AAC AAG TCC GAG TGT CAC AAT CAA	4214
	Asn Val Asn Ser Thr Met Val Asn Asn Lys Ser Glu Cys His Asn Gln	
	1325 1330 1335	
75	AAC AGC ACC GGC CAC TTC TTC TGG GTC AAC GTC AAA GTC AAC TTC GAC	4262
	Asn Ser Thr Gly His Phe Phe Trp Val Asn Val Lys Val Asn Phe Asp	
	1340 1345 1350	

	AAC	CTC	GCT	ATG	GGC	TAC	CTC	GCA	CTT	CTT	CAG	GTG	GCA	ACC	TTC	AAA	4310
	Asn	Val	Ala	Met	Gly	Tyr	Leu	Ala	Leu	Leu	Gln	Val	Ala	Thr	Phe	Lys	
	1355						1360					1365					
5	GGC	TGG	ATG	GAC	ATA	ATG	TAT	GCA	GCT	GTT	GAT	TCC	GGA	GAG	ATC	AAC	4358
	Gly	Trp	Met	Asp	Ile	Met	Tyr	Ala	Ala	Val	Asp	Ser	Gly	Glu	Ile	Asn	
	1370					1375					1380					1385	
10	AGT	CAG	CCT	AAC	TGG	GAG	AAC	AAC	TTG	TAC	ATG	TAC	CTG	TAC	TTC	GTC	4406
	Ser	Gln	Pro	Asn	Trp	Glu	Asn	Asn	Leu	Tyr	Met	Tyr	Leu	Tyr	Phe	Val	
					1390					1395					1400		
15	GTT	TTC	ATC	ATT	TTC	GGT	GGC	TTC	TTC	ACG	CTG	AAT	CTC	TTT	GTT	GGG	4454
	Val	Phe	Ile	Ile	Phe	Gly	Gly	Phe	Phe	Thr	Leu	Asn	Leu	Phe	Val	Gly	
				1405					1410					1415			
20	GTC	ATA	ATC	GAC	AAC	TTC	AAC	CAA	CAG	AAA	AAA	AAG	CTA	GGA	GGC	CAG	4502
	Val	Ile	Ile	Asp	Asn	Phe	Asn	Gln	Gln	Lys	Lys	Lys	Leu	Gly	Gly	Gln	
			1420					1425					1430				
25	GAC	ATC	TTC	ATG	ACA	GAA	GAG	CAG	AAG	AAG	TAC	TAC	AAT	GCC	ATG	AAG	4550
	Asp	Ile	Phe	Met	Thr	Glu	Glu	Gln	Lys	Lys	Tyr	Tyr	Asn	Ala	Met	Lys	
	1435					1440					1445						
30	AAG	CTG	GGC	TCC	AAG	AAA	CCC	CAG	AAG	CCC	ATC	CCA	CGG	CCC	CTG	AAT	4598
	Lys	Leu	Gly	Ser	Lys	Lys	Pro	Gln	Lys	Pro	Ile	Pro	Arg	Pro	Leu	Asn	
	1450					1455					1460					1465	
35	AAG	TAC	CAA	GGC	TTC	GTG	TTT	GAC	ATC	GTG	ACC	AGG	CAA	GCC	TTT	GAC	4646
	Lys	Tyr	Gln	Gly	Phe	Val	Phe	Asp	Ile	Val	Thr	Arg	Gln	Ala	Phe	Asp	
				1470						1475					1480		
40	ATC	ATC	ATC	ATG	GTT	CTC	ATC	TGC	CTC	AAC	ATG	ATC	ACC	ATG	ATG	GTG	4694
	Ile	Ile	Ile	Met	Val	Leu	Ile	Cys	Leu	Asn	Met	Ile	Thr	Met	Met	Val	
				1485				1490						1495			
45	GAG	ACC	GAC	GAG	CAG	GGC	GAG	GAG	AAG	ACG	AAG	GTT	CTG	GGC	AGA	ATC	4742
	Glu	Thr	Asp	Glu	Gln	Gly	Glu	Glu	Lys	Thr	Lys	Val	Leu	Gly	Arg	Ile	
			1500				1505						1510				
50	AAC	CAG	TTC	TTT	GTG	GCC	GTC	TTC	ACG	GGC	GAG	TGT	GTG	ATG	AAG	ATG	4790
	Asn	Gln	Phe	Phe	Val	Ala	Val	Phe	Thr	Gly	Glu	Cys	Val	Met	Lys	Met	
	1515					1520					1525						
55	TTC	GCC	CTG	CGA	CAG	TAC	TAC	TTC	ACC	AAC	GGC	TGG	AAC	GTG	TTC	GAC	4838
	Phe	Ala	Leu	Arg	Gln	Tyr	Tyr	Phe	Thr	Asn	Gly	Trp	Asn	Val	Phe	Asp	
	1530					1535					1540				1545		
60	TTC	ATA	GTG	GTG	ATC	CTG	TCC	ATT	GGG	AGT	CTG	CTG	TTT	TCT	GCA	ATC	4886
	Phe	Ile	Val	Val	Ile	Leu	Ser	Ile	Gly	Ser	Leu	Leu	Phe	Ser	Ala	Ile	
					1550				1555						1560		
65	CTT	AAG	TCA	CTG	GAA	AAC	TAC	TTC	TCC	CCG	ACG	CTC	TTC	CGG	GTC	ATC	4934
	Leu	Lys	Ser	Leu	Glu	Asn	Tyr	Phe	Ser	Pro	Thr	Leu	Phe	Arg	Val	Ile	
				1565				1570						1575			
70	CGT	CTG	GCC	AGG	ATC	GGC	CGC	ATC	CTC	AGG	CTG	ATC	CGA	GCA	GCC	AAG	4982
	Arg	Leu	Ala	Arg	Ile	Gly	Arg	Ile	Leu	Arg	Leu	Ile	Arg	Ala	Ala	Lys	
			1580				1585					1590					
75	GGG	ATT	CGC	ACG	CTG	CTC	TTC	GCC	CTC	ATG	ATG	TCC	CTG	CCC	GCC	CTC	5030
	Gly	Ile	Arg	Thr	Leu	Leu	Phe	Ala	Leu	Met	Met	Ser	Leu	Pro	Ala	Leu	
	1595						1600					1605					

	TTC AAC ATC GGC CTC CTC CTC TTC CTC GTC ATG TTC ATC TAC TCC ATC	5078
	Phe Asn Ile Gly Leu Leu Leu Phe Leu Val Met Phe Ile Tyr Ser Ile	
	1610 1615 1620 1625	
5	TTC GGC ATG GCC AGC TTC GCT AAC GTC GTG GAC GAG GCC GGC ATC GAC	5126
	Phe Gly Met Ala Ser Phe Ala Asn Val Val Asp Glu Ala Gly Ile Asp	
	1630 1635 1640	
10	GAC ATG TTC AAC TTC AAG ACC TTT GGC AAC AGC ATG CTG TGC CTG TTC	5174
	Asp Met Phe Asn Phe Lys Thr Phe Gly Asn Ser Met Leu Cys Leu Phe	
	1645 1650 1655	
15	CAG ATC ACC ACC TCG GCC GGC TGG GAC GGC CTC CTC AGC CCC ATC CTC	5222
	Gln Ile Thr Thr Ser Ala Gly Trp Asp Gly Leu Leu Ser Pro Ile Leu	
	1660 1665 1670	
	AAC ACG GGG CCT CCC TAC TGC GAC CCC AAC CTG CCC AAC AGC AAC GGC	5270
	Asn Thr Gly Pro Pro Tyr Cys Asp Pro Asn Leu Pro Asn Ser Asn Gly	
	1675 1680 1685	
20	TCC CGG GGG AAC TGC GGG AGC CCG GCG GTG GGC ATC ATC TTC TTC ACC	5318
	Ser Arg Gly Asn Cys Gly Ser Pro Ala Val Gly Ile Ile Phe Phe Thr	
	1690 1695 1700 1705	
25	ACC TAC ATC ATC ATC TCC TTC CTC ATC GTG GTC AAC ATG TAC ATC GCA	5366
	Thr Tyr Ile Ile Ile Ser Phe Leu Ile Val Val Asn Met Tyr Ile Ala	
	1710 1715 1720	
30	GTG ATT CTG GAG AAC TTC AAC GTA GCC ACC GAG GAG AGC ACG GAG CCC	5414
	Val Ile Leu Glu Asn Phe Asn Val Ala Thr Glu Glu Ser Thr Glu Pro	
	1725 1730 1735	
35	CTG AGC GAG GAC GAC TTC GAC ATG TTC TAT GAG ACC TGG GAG AAG TTC	5462
	Leu Ser Glu Asp Asp Phe Asp Met Phe Tyr Glu Thr Trp Glu Lys Phe	
	1740 1745 1750	
	GAC CCG GAG GCC ACC CAG TTC ATT GCC TTT TCT GCC CTC TCA GAC TTC	5510
	Asp Pro Glu Ala Thr Gln Phe Ile Ala Phe Ser Ala Leu Ser Asp Phe	
	1755 1760 1765	
40	GCG GAC ACG CTC TCC GGC CCT CTT AGA ATC CCC AAA CCC AAC CAG AAT	5558
	Ala Asp Thr Leu Ser Gly Pro Leu Arg Ile Pro Lys Pro Asn Gln Asn	
	1770 1775 1780 1785	
45	ATA TTA ATC CAG ATG GAC CTG CCG TTG GTC CCC GGG GAT AAG ATC CAC	5606
	Ile Leu Ile Gln Met Asp Leu Pro Leu Val Pro Gly Asp Lys Ile His	
	1790 1795 1800	
50	TGT CTG GAC ATC CTT TTT GCC TTC ACA AAG AAC GTC TTG GGA GAA TCC	5654
	Cys Leu Asp Ile Leu Phe Ala Phe Thr Lys Asn Val Leu Gly Glu Ser	
	1805 1810 1815	
55	GGG GAG TTG GAC TCC CTG AAG ACC AAT ATG GAA GAG AAG TTT ATG GCG	5702
	Gly Glu Leu Asp Ser Leu Lys Thr Asn Met Glu Glu Lys Phe Met Ala	
	1820 1825 1830	
	ACC AAT CTC TCC AAA GCA TCC TAT GAA CCA ATA GCC ACC ACC CTC CGG	5750
	Thr Asn Leu Ser Lys Ala Ser Tyr Glu Pro Ile Ala Thr Thr Leu Arg	
	1835 1840 1845	
60	TGG AAG CAG GAA GAC CTC TCA GCC ACA GTC ATT CAA AAG GCC TAC CGG	5798
	Trp Lys Gln Glu Asp Leu Ser Ala Thr Val Ile Gln Lys Ala Tyr Arg	
	1850 1855 1860 1865	

AGC TAC ATG CTG CAC CGC TCC TTG ACA CTC TCC AAC ACC CTG CAT GTG 5846
 Ser Tyr Met Leu His Arg Ser Leu Thr Leu Ser Asn Thr Leu His Val
 1870 1875 1880

5 CCC AGG GCT GAG GAG GAT GGC GTG TCA CTT CCC GGG GAA GGC TAC AGT 5894
 Pro Arg Ala Glu Glu Asp Gly Val Ser Leu Pro Gly Glu Gly Tyr Ser
 1885 1890 1895

10 ACA TTC ATG GCA AAC AGT GGA CTC CCG GAC AAA TCA GAA ACT GCC TCT 5942
 Thr Phe Met Ala Asn Ser Gly Leu Pro Asp Lys Ser Glu Thr Ala Ser
 1900 1905 1910

15 GCT ACG TCT TTC CCG CCA TCC TAT GAC AGT GTC ACC AGG GGC CTG AGT 5990
 Ala Thr Ser Phe Pro Pro Ser Tyr Asp Ser Val Thr Arg Gly Leu Ser
 1915 1920 1925

GAC CGG GCC AAC ATT AAC CCA TCT AGC TCA ATG CAA AAT GAA GAT GAG 6038
 Asp Arg Ala Asn Ile Asn Pro Ser Ser Ser Met Gln Asn Glu Asp Glu
 1930 1935 1940 1945

20 GTC GCT GCT AAG GAA GGA AAC AGC CCT GGA CCT CAG TGAAGGCACT 6084
 Val Ala Ala Lys Glu Gly Asn Ser Pro Gly Pro Gln
 1950 1955

25 CAGGCATGCA CAGGGCAGGT TCCAATGTCT TTCTCTGCTG TACTAACTCC TTCCCTCTGG 6144

AGGTGGCACC AACCTCCAGC CTCCACCAAT GCATGTCACT GGTCATGGTG TCAGAACTGA 6204

30 ATGGGGACAT CCTTGAGAAA GCCCCACCC CAATAGGAAT CAAAAGCCAA GGATACTCCT 6264

CCATTCTGAC GTCCCTTCCG AGTTCCCAGA AGATGTGATT GCTCCCTTCT GTTTGTGACC 6324

AGAGACGTGA TTCACCAACT TCTCGGAGCC AGAGACACAT AGCAAAGACT TTTCTGCTGG 6384

35 TGTCGGGCAG TCTTAGAGAA GTCACGTAGG GGTGTTGACT GAGAATTAGG GTTTGCATGA 6444

CTGCATGCTC ACAGCTGCCG GACAATACCT GTGAGTCGGC CATTAAAATT AATATTTTAA 6504

40 AAGTTAAAAA AAAAAAAAAA AAA 6527

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1957 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met Glu Leu Pro Phe Ala Ser Val Gly Thr Thr Asn Phe Arg Arg Phe
 1 5 10

55 Thr Pro Glu Ser Leu Ala Glu Ile Glu Lys Gln Ile Ala Ala His Arg
 20 25 30

60 Ala Ala Lys Lys Ala Arg Thr Lys His Arg Gly Gln Glu Asp Lys Gly
 35 40 45

Glu Lys Pro Arg Pro Gln Leu Asp Leu Lys Asp Cys Asn Gln Leu Pro
 50 55 60

Lys Phe Tyr Gly Glu Leu Pro Ala Glu Leu Val Gly Glu Pro Leu Glu
 65 70 75 80
 5 Asp Leu Asp Pro Phe Tyr Ser Thr His Arg Thr Phe Met Val Leu Asn
 85 90 95
 Lys Ser Arg Thr Ile Ser Arg Phe Ser Ala Thr Trp Ala Leu Trp Leu
 100 105 110
 10 Phe Ser Pro Phe Asn Leu Ile Arg Arg Thr Ala Ile Lys Val Ser Val
 115 120 125
 His Ser Trp Phe Ser Ile Phe Ile Thr Ile Thr Ile Leu Val Asn Cys
 130 135 140
 15 Val Cys Met Thr Arg Thr Asp Leu Pro Glu Lys Val Glu Tyr Val Phe
 145 150 155 160
 Thr Val Ile Tyr Thr Phe Glu Ala Leu Ile Lys Ile Leu Ala Arg Gly
 165 170 175
 Phe Cys Leu Asn Glu Phe Thr Tyr Leu Arg Asp Pro Trp Asn Trp Leu
 180 185 190
 25 Asp Phe Ser Val Ile Thr Leu Ala Tyr Val Gly Ala Ala Ile Asp Leu
 195 200 205
 Arg Gly Ile Ser Gly Leu Arg Thr Phe Arg Val Leu Arg Ala Leu Lys
 210 215 220
 30 Thr Val Ser Val Ile Pro Gly Leu Lys Val Ile Val Gly Ala Leu Ile
 225 230 235 240
 His Ser Val Arg Lys Leu Ala Asp Val Thr Ile Leu Thr Val Phe Cys
 245 250 255
 Leu Ser Val Phe Ala Leu Val Gly Leu Gln Leu Phe Lys Gly Asn Leu
 260 265 270
 40 Lys Asn Lys Cys Ile Arg Asn Gly Thr Asp Pro His Lys Ala Asp Asn
 275 280 285
 Leu Ser Ser Glu Met Ala Glu Tyr Ile Phe Ile Lys Pro Gly Thr Thr
 290 295 300
 45 Asp Pro Leu Leu Cys Gly Asn Gly Ser Asp Ala Gly His Cys Pro Gly
 305 310 315 320
 Gly Tyr Val Cys Leu Lys Thr Pro Asp Asn Pro Asp Phe Asn Tyr Thr
 325 330 335
 50 Ser Phe Asp Ser Phe Ala Trp Ala Phe Leu Ser Leu Phe Arg Leu Met
 340 345 350
 55 Thr Gln Asp Ser Trp Glu Arg Leu Tyr Gln Gln Thr Leu Arg Ala Ser
 355 360 365
 Gly Lys Met Tyr Met Val Phe Phe Val Leu Val Ile Phe Leu Gly Ser
 370 375 380
 60 Phe Tyr Leu Val Asn Leu Ile Leu Ala Val Val Thr Met Ala Tyr Glu
 385 390 395 400

Glu Gln Ser Gln Ala Thr Ile Ala Glu Ile Glu Ala Lys Glu Lys Lys
 405 410 415
 5 Phe Gln Glu Ala Leu Glu Val Leu Gln Lys Glu Gln Glu Val Leu Ala
 420 425 430
 Ala Leu Gly Ile Asp Thr Thr Ser Leu Gln Ser His Ser Gly Ser Pro
 435 440 445
 10 Leu Ala Ser Lys Asn Ala Asn Glu Arg Arg Pro Arg Val Lys Ser Arg
 450 455 460
 Val Ser Glu Gly Ser Thr Asp Asp Asn Arg Ser Pro Gln Ser Asp Pro
 465 470 475 480
 15 Tyr Asn Gln Arg Arg Met Ser Phe Leu Gly Leu Ser Ser Gly Arg Arg
 485 490 495
 Arg Ala Ser His Gly Ser Val Phe His Phe Arg Ala Pro Ser Gln Asp
 500 505 510
 Ile Ser Phe Pro Asp Gly Ile Thr Pro Asp Asp Gly Val Phe His Gly
 515 520 525
 25 Asp Gln Glu Ser Arg Arg Gly Ser Ile Leu Leu Gly Arg Gly Ala Gly
 530 535 540
 Gln Thr Gly Pro Leu Pro Arg Ser Pro Leu Pro Gln Ser Pro Asn Pro
 545 550 555 560
 30 Gly Arg Arg His Gly Glu Glu Gly Gln Leu Gly Val Pro Thr Gly Glu
 565 570 575
 Leu Thr Ala Gly Ala Pro Glu Gly Pro Ala Leu Asp Thr Thr Gly Gln
 580 585 590
 35 Lys Ser Phe Leu Ser Ala Gly Tyr Leu Asn Glu Pro Phe Arg Ala Gln
 595 600 605
 40 Arg Ala Met Ser Val Val Ser Ile Met Thr Ser Val Ile Glu Glu Leu
 610 615 620
 Glu Glu Ser Lys Leu Lys Cys Pro Pro Cys Leu Ile Ser Phe Ala Gln
 625 630 635 640
 45 Lys Tyr Leu Ile Trp Glu Cys Cys Pro Lys Trp Arg Lys Phe Lys Met
 645 650 655
 Ala Leu Phe Glu Leu Val Thr Asp Pro Phe Ala Glu Leu Thr Ile Thr
 660 665 670
 50 Leu Cys Ile Val Val Asn Thr Val Phe Met Ala Met Glu His Tyr Pro
 675 680 685
 55 Met Thr Asp Ala Phe Asp Ala Met Leu Gln Ala Gly Asn Ile Val Phe
 690 695 700
 Thr Val Phe Phe Thr Met Glu Met Ala Phe Lys Ile Ile Ala Phe Asp
 705 710 715 720
 60 Pro Tyr Tyr Tyr Phe Gln Lys Lys Trp Asn Ile Phe Asp Cys Val Ile
 725 730 735

Val Thr Val Ser Leu Leu Glu Leu Ser Ala Ser Lys Lys Gly Ser Leu
740 745 750

5 Ser Val Leu Arg Ser Leu Arg Leu Leu Arg Val Phe Lys Leu Ala Lys
755 760 765

Ser Trp Pro Thr Deu Asn Thr Leu Ile Lys Ile Ile Gly Asn Ser Val
770 775 780

10 Gly Ala Leu Gly Asn Leu Thr Phe Ile Leu Ala Ile Ile Val Phe Ile
785 790 795 800

Phe Ala Leu Val Gly Lys Gln Leu Leu Ser Glu Asp Tyr Gly Cys Arg
805 810 815

15 Lys Asp Gly Val Ser Val Trp Asn Gly Glu Lys Leu Arg Trp His Met
820 825 830

Cys Asp Phe Phe His Ser Phe Leu Val Val Phe Arg Ile Leu Cys Gly
835 840 845

Glu Trp Ile Glu Asn Met Trp Val Cys Met Glu Val Ser Gln Lys Ser
850 855 860

25 Ile Cys Leu Ile Leu Phe Leu Thr Val Met Val Leu Gly Asn Leu Val
865 870 875 880

Val Leu Asn Leu Phe Ile Ala Leu Leu Leu Asn Ser Phe Ser Ala Asp
885 890 895

30 Asn Leu Thr Ala Pro Glu Asp Asp Gly Glu Val Asn Asn Leu Gln Leu
900 905 910

Ala Leu Ala Arg Ile Gln Val Leu Gly His Arg Ala Ser Arg Ala Ile
915 920 925

Ala Ser Tyr Ile Ser Ser His Cys Arg Phe Arg Trp Pro Lys Val Glu
930 935 940

40 Thr Gln Leu Gly Met Lys Pro Pro Leu Thr Ser Ser Glu Ala Lys Asn
945 950 955 960

His Ile Ala Thr Asp Ala Val Ser Ala Ala Val Gly Asn Leu Thr Lys
965 970 975

45 Pro Ala Leu Ser Ser Pro Lys Glu Asn His Gly Asp Phe Ile Thr Asp
980 985 990

Pro Asn Val Trp Val Ser Val Pro Ile Ala Glu Gly Glu Ser Asp Leu
995 1000 1005

50 Asp Glu Leu Glu Glu Asp Met Glu Gln Ala Ser Gln Ser Ser Trp Gln
1010 1015 1020

55 Glu Glu Asp Pro Lys Gly Gln Gln Glu Gln Leu Pro Gln Val Gln Lys
1025 1030 1035 1040

Cys Glu Asn His Gln Ala Ala Arg Ser Pro Ala Ser Met Met Ser Ser
1045 1050 1055

60 Glu Asp Leu Ala Pro Tyr Leu Gly Glu Ser Trp Lys Arg Lys Asp Ser
1060 1065 1070

Pro Gln Val Pro Ala Glu Gly Val Asp Asp Thr Ser Ser Ser Glu Gly
1075 1080 1085

5 Ser Thr Val Asp Cys Pro Asp Pro Glu Glu Ile Leu Arg Lys Ile Pro
1090 1095 1100

Glu Leu Ala Asp Asp Leu Asp Glu Pro Asp Asp Cys Phe Thr Glu Gly
1105 1110 1115 1120

10 Cys Thr Arg Arg Cys Pro Cys Cys Asn Val Asn Thr Ser Lys Ser Pro
1125 1130 1135

Trp Ala Thr Gly Trp Gln Val Arg Lys Thr Cys Tyr Arg Ile Val Glu
1140 1145 1150

15 His Ser Trp Phe Glu Ser Phe Ile Ile Phe Met Ile Leu Leu Ser Ser
1155 1160 1165

Gly Ala Leu Ala Phe Glu Asp Asn Tyr Leu Glu Glu Lys Pro Arg Val
1170 1175 1180

Lys Ser Val Leu Glu Tyr Thr Asp Arg Val Phe Thr Phe Ile Phe Val
1185 1190 1195 1200

25 Phe Glu Met Leu Leu Lys Trp Val Ala Tyr Gly Phe Lys Lys Tyr Phe
1205 1210 1215

Thr Asn Ala Trp Cys Trp Leu Asp Phe Leu Ile Val Asn Ile Ser Leu
1220 1225 1230

30 Thr Ser Leu Ile Ala Lys Ile Leu Glu Tyr Ser Asp Val Ala Ser Ile
1235 1240 1245

Lys Ala Leu Arg Thr Leu Arg Ala Leu Arg Pro Leu Arg Ala Leu Ser
1250 1255 1260

Arg Phe Glu Gly Met Arg Val Val Val Asp Ala Leu Val Gly Ala Ile
1265 1270 1275 1280

40 Pro Ser Ile Met Asn Val Leu Leu Val Cys Leu Ile Phe Trp Leu Ile
1285 1290 1295

Phe Ser Ile Met Gly Val Asn Leu Phe Ala Gly Lys Phe Ser Lys Cys
1300 1305 1310

45 Val Asp Thr Arg Asn Asn Pro Phe Ser Asn Val Asn Ser Thr Met Val
1315 1320 1325

Asn Asn Lys Ser Glu Cys His Asn Gln Asn Ser Thr Gly His Phe Phe
1330 1335 1340

Trp Val Asn Val Lys Val Asn Phe Asp Asn Val Ala Met Gly Tyr Leu
1345 1350 1355 1360

55 Ala Leu Leu Gln Val Ala Thr Phe Lys Gly Trp Met Asp Ile Met Tyr
1365 1370 1375

Ala Ala Val Asp Ser Gly Glu Ile Asn Ser Gln Pro Asn Trp Glu Asn
1380 1385 1390

60 Asn Leu Tyr Met Tyr Leu Tyr Phe Val Val Phe Ile Ile Phe Gly Gly
1395 1400 1405

Phe Phe Thr Leu Asn Leu Phe Val Gly Val Ile Ile Asp Asn Phe Asn
 1410 1415 1420
 5 Gln Gln Lys Lys Lys Leu Gly Gly Gln Asp Ile Phe Met Thr Glu Glu
 1425 1430 1435 1440
 Gln Lys Lys Tyr Tyr Asn Ala Met Lys Lys Leu Gly Ser Lys Lys Pro
 1445 1450 1455
 10 Gln Lys Pro Ile Pro Arg Pro Leu Asn Lys Tyr Gln Gly Phe Val Phe
 1460 1465 1470
 Asp Ile Val Thr Arg Gln Ala Phe Asp Ile Ile Ile Met Val Leu Ile
 1475 1480 1485
 15 Cys Leu Asn Met Ile Thr Met Met Val Glu Thr Asp Glu Gln Gly Glu
 1490 1495 1500
 20 Glu Lys Thr Lys Val Leu Gly Arg Ile Asn Gln Phe Phe Val Ala Val
 1505 1510 1515 1520
 Phe Thr Gly Glu Cys Val Met Lys Met Phe Ala Leu Arg Gln Tyr Tyr
 1525 1530 1535
 25 Phe Thr Asn Gly Trp Asn Val Phe Asp Phe Ile Val Val Ile Leu Ser
 1540 1545 1550
 Ile Gly Ser Leu Leu Phe Ser Ala Ile Leu Lys Ser Leu Glu Asn Tyr
 1555 1560 1565
 30 Phe Ser Pro Thr Leu Phe Arg Val Ile Arg Leu Ala Arg Ile Gly Arg
 1570 1575 1580
 Ile Leu Arg Leu Ile Arg Ala Ala Lys Gly Ile Arg Thr Leu Leu Phe
 1585 1590 1595 1600
 Ala Leu Met Met Ser Leu Pro Ala Leu Phe Asn Ile Gly Leu Leu Leu
 1605 1610 1615
 40 Phe Leu Val Met Phe Ile Tyr Ser Ile Phe Gly Met Ala Ser Phe Ala
 1620 1625 1630
 Asn Val Val Asp Glu Ala Gly Ile Asp Asp Met Phe Asn Phe Lys Thr
 1635 1640 1645
 45 Phe Gly Asn Ser Met Leu Cys Leu Phe Gln Ile Thr Thr Ser Ala Gly
 1650 1655 1660
 Trp Asp Gly Leu Leu Ser Pro Ile Leu Asn Thr Gly Pro Pro Tyr Cys
 1665 1670 1675 1680
 Asp Pro Asn Leu Pro Asn Ser Asn Gly Ser Arg Gly Asn Cys Gly Ser
 1685 1690 1695
 55 Pro Ala Val Gly Ile Ile Phe Phe Thr Thr Tyr Ile Ile Ile Ser Phe
 1700 1705 1710
 Leu Ile Val Val Asn Met Tyr Ile Ala Val Ile Leu Glu Asn Phe Asn
 1715 1720 1725
 60 Val Ala Thr Glu Glu Ser Thr Glu Pro Leu Ser Glu Asp Asp Phe Asp
 1730 1735 1740

Met Phe Tyr Glu Thr Trp Glu Lys Phe Asp Pro Glu Ala Thr Gln Phe
1745 1750 1755 1760
5 Ile Ala Phe Ser Ala Leu Ser Asp Phe Ala Asp Thr Leu Ser Gly Pro
1765 1770 1775
Leu Arg Ile Pro Lys Pro Asn Gln Asn Ile Leu Ile Gln Met Asp Leu
1780 1785 1790
10 Pro Leu Val Pro Gly Asp Lys Ile His Cys Leu Asp Ile Leu Phe Ala
1795 1800 1805
Phe Thr Lys Asn Val Leu Gly Glu Ser Gly Glu Leu Asp Ser Leu Lys
1810 1815 1820
15 Thr Asn Met Glu Glu Lys Phe Met Ala Thr Asn Leu Ser Lys Ala Ser
1825 1830 1835 1840
Tyr Glu Pro Ile Ala Thr Thr Leu Arg Trp Lys Gln Glu Asp Leu Ser
1845 1850 1855
Ala Thr Val Ile Gln Lys Ala Tyr Arg Ser Tyr Met Leu His Arg Ser
1860 1865 1870
25 Leu Thr Leu Ser Asn Thr Leu His Val Pro Arg Ala Glu Glu Asp Gly
1875 1880 1885
Val Ser Leu Pro Gly Glu Gly Tyr Ser Thr Phe Met Ala Asn Ser Gly
1890 1895 1900
30 Leu Pro Asp Lys Ser Glu Thr Ala Ser Ala Thr Ser Phe Pro Pro Ser
1905 1910 1915 1920
Tyr Asp Ser Val Thr Arg Gly Leu Ser Asp Arg Ala Asn Ile Asn Pro
1925 1930 1935
35 Ser Ser Ser Met Gln Asn Glu Asp Glu Val Ala Ala Lys Glu Gly Asn
1940 1945 1950
40 Ser Pro Gly Pro Gln
1955

(2) INFORMATION FOR SEQ ID NO:9:

- 45 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
50 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

CAGCTTCGCT CAGAAGTATC T

60

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

TTCTCGCCGT TCCACACGGA GA

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Phe Arg Leu Met
1

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 9 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Thr Gln Asp Phe Trp Glu Asn Leu Tyr
1 5

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 9 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Thr Gln Asp Tyr Trp Glu Asn Leu Tyr
1 5

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 9 amino acids

22

(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

10 Thr Gln Asp Cys Trp Glu Arg Leu Tyr
1 5

(2) INFORMATION FOR SEQ ID NO:15:

15 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 9 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

20 (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

25

Thr Gln Asp Ser Trp Glu Arg Leu Tyr
1 5

(2) INFORMATION FOR SEQ ID NO:16:

30

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 9 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

35

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

40

Thr Gln Asp Phe Trp Glu Arg Leu Tyr
1 5

(2) INFORMATION FOR SEQ ID NO:17:

45

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

50

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

55

Thr Gln Asp Ser Trp Glu Arg
1 5

60

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids

(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

10 Gly Ser Thr Asp Asp Asn Arg Ser Pro Gln Ser Asp Pro Tyr Asn
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 10 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

25 Ser Pro Lys Glu Asn His Gly Asp Phe Ile
1 5 10

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 9 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

40 Pro Asn His Asn Gly Ser Arg Gly Asn
1 5

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

55 Arg Leu Leu Arg Val Phe Lys Leu Ala Lys Ser Trp Pro Thr Leu
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

5 (ii) MOLECULE TYPE: cDNA

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

GCTTGCTGCG GGTCTTCAAG C

21

(2) INFORMATION FOR SEQ ID NO:23:

15 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 14 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

20 (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

25 Leu Arg Ala Leu Pro Leu Arg Ala Leu Ser Arg Phe Glu Gly
1 5 10

(2) INFORMATION FOR SEQ ID NO:24:

30 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

35 (ii) MOLECULE TYPE: cDNA

40 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

ATCGAGACAG AGCCCGCAGC G

21

(2) INFORMATION FOR SEQ ID NO:25:

45 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 44 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
50 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

ACGGGTGCCG CAAGGACGGC GTCTCCGTGT GGAACGGCGA GAAG

44

60 (2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 45 base pairs
(B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

5

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

10 GGCTATCCTT CCTCTTCCAG CTCTCACCCA GGTATGGAGC CAGGT

45

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

15

(A) LENGTH: 21 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

20

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

25

TCCCGTACGC TGCAGCTCTT T

21

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

30

(A) LENGTH: 15 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

35

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

40

CCCGGGAAG GCTAC

15

(2) INFORMATION FOR SEQ ID NO:29:

45

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

55

GTCGACACCA GAAAT

15

(2) INFORMATION FOR SEQ ID NO:30:

60

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 30 base pairs
(B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

5 (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:
10 GGATCCTCTA GAGTCGACCT GCAGAAGGAA 30

(2) INFORMATION FOR SEQ ID NO:31:

15 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

20 (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:
25 TGACGCAGGA CTCCTGGGAG CGCC 24



CERTIFICATE OF MAILING (37 CFR 1.8 (a))

I hereby certify that the attached papers or fee is being deposited with the United States Postal Service on the date shown below with sufficient postage as first class mail in an envelope addressed to the: Assistant Commissioner For Patents, Washington, D.C. 20231.

January 21, 1997
(Date)

LIZA D. HOHENSCHUTZ
(Printed Name)

Liza D. Hohenschutz
(Signature)

ZENECA Inc.
Docket No. 70086

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Application of: WOOD ET AL.

Serial Number: 08\669,656

Group Art Unit:

Filed: JUNE 24, 1996

Examiner:

For: ION CHANNEL

Assistant Commissioner for Patents
Washington, D.C. 20231

Sir:

COVER LETTER

Transmitted herewith are the following:

- ☐ Response to Office Action.
- ☐ Petition for extension of time (37 CFR 1.136).
- ☒ Information Disclosure Statement.
- ☒ Information Disclosure Citation by Applicant (Form PTO-1449)
- ☐ Appeal Brief (in triplicate).
- ☐ Issue Fee (Forms PTOL -85B and -85C).
- ☒ 2 References

The items checked below are appropriate:

1. ☒ It is believed that no fee is due as a result of this transmittal.

2. (X) The Commissioner is hereby authorized to charge any additional fees which may be required or to credit any overpayment to Deposit Account No. 26-0166. This sheet is enclosed in duplicate.

Respectfully submitted,

ZENECA Inc.

Dated: *January 21, 1997*

ZENECA Inc.
Docket No. 70086
y:\ldh\70086\0117cov.doc

By: *Liza D. Hohenschutz*
Liza D. Hohenschutz
Attorney for Applicants
Reg. No. 33,712
Telephone: 302/886-7466



Application No.: 08669,652

NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS CONTAINING
NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE DISCLOSURES

The nucleotide and/or amino acid sequence disclosure contained in this application does not comply with the requirements for such a disclosure as set forth in 37 C.F.R. 1.821 - 1.825 for the following reason(s):

- ☒ 1. This application clearly fails to comply with the requirements of 37 C.F.R. 1.821-1.825. Applicant's attention is directed to these regulations, published at 1114 OG 29, May 15, 1990 and at 55 FR 18230, May 1, 1990.
- ☐ 2. This application does not contain, as a separate part of the disclosure on paper copy, a "Sequence Listing" as required by 37 C.F.R. 1.821(c).
- ☐ 3. A copy of the "Sequence Listing" in computer readable form has not been submitted as required by 37 C.F.R. 1.821(e).
- ☐ 4. A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 C.F.R. 1.822 and/or 1.823, as indicated on the attached copy of the marked -up "Raw Sequence Listing."
- ☐ 5. The computer readable form that has been filed with this application has been found to be damaged and/or unreadable as indicated on the attached CRF Diskette Problem Report. A Substitute computer readable form must be submitted as required by 37 C.F.R. 1.825(d).
- ☐ 6. The paper copy of the "Sequence Listing" is not the same as the computer readable form of the "Sequence Listing" as required by 37 C.F.R. 1.821(e).
- ☐ 7. Other: _____

Applicant Must Provide:

- ☒ An initial or substitute computer readable form (CRF) copy of the "Sequence Listing".
- ☒ An initial or substitute paper copy of the "Sequence Listing", as well as an amendment directing its entry into the specification.
- ☒ A statement that the content of the paper and computer readable copies are the same and, where applicable, include no new matter, as required by 37 C.F.R. 1.821(e) or 1.821(f) or 1.821(g) or 1.825(b) or 1.825(d).

For questions regarding compliance to these requirements, please contact:

For Rules Interpretation, call (703) 308-4216

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